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OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 05:48:35 ; Search time 370 Seconds
 (without alignments)

6337.256 Million cell updates/sec

Title: US-10-089-543-2

Perfect score: 1433
 Sequence: 1 actataggccacgcgtggtc.....tgagagaattcctcacatc 1433

Scoring table: IDENTITY_NUC
 GapOp 10.0 , GapExt 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : Issued Patents NA:*

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 3: /cgm2_6/prodata/1/ina/6A_COMB.seq.*
 4: /cgm2_6/prodata/1/ina/6B_COMB.seq.*
 5: /cgm2_6/prodata/1/ina/PCFTUS_COMB.seq.*
 6: /cgm2_6/prodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Match Length	DB ID	Description
1	113.8	7.9	31491	3 US-09-16-186-1	Sequence 1, Appli
2	113.8	7.9	31491	4 US-09-864-880A-1	Sequence 1, Appli
c 3	101.8	7.1	612	4 US-09-902-540-1357	Sequence 1357, Ap
c 4	6.3	59519	4	US-09-16-1504	Sequence 13504, A
c 5	88.8	6.2	55886	4 US-09-949-016-15129	Sequence 15129, A
c 6	88.4	6.2	19124	2 US-08-487-926B-13	Sequence 15831, A
c 7	88.4	6.2	205044	4 US-09-949-016-15851	Sequence 15851, A
c 8	88.4	6.2	205044	4 US-09-949-016-15852	Sequence 15852, A
c 9	88.4	6.2	205044	4 US-09-949-016-15853	Sequence 15853, A
c 10	88.4	6.2	223471	4 US-09-949-016-1387	Sequence 12387, A
c 11	88.4	6.2	223471	4 US-09-949-016-12724	Sequence 12724, A
c 12	88.4	6.2	223471	4 US-09-949-016-12725	Sequence 12725, A
c 13	87.4	6.1	61178	4 US-09-949-016-17369	Sequence 17369, A
c 14	85.8	6.0	187169	4 US-09-949-016-1276	Sequence 12776, A
c 15	85.8	6.0	191569	4 US-09-949-016-15940	Sequence 15940, A
c 16	84.4	5.9	1039	4 US-09-949-016-12880	Sequence 12880, Ap
c 17	84.2	5.9	263693	4 US-09-949-016-13386	Sequence 13386, A
c 18	84.2	5.9	263694	4 US-09-949-016-16915	Sequence 16915, A
c 19	84	5.9	20674	3 US-09-54-638-651	Sequence 651, App
c 20	84	5.9	147382	4 US-10-170-057-651	Sequence 651, App
c 21	83.8	5.8	147382	4 US-09-949-016-14624	Sequence 14624, A
c 22	83.6	5.8	601	4 US-09-949-016-30531	Sequence 30531, A
c 23	83.6	5.8	601	4 US-09-949-016-30531	Sequence 30531, A
c 24	83.6	5.8	601	4 US-09-949-016-37149	Sequence 37149, A
c 25	83.6	5.8	601	4 US-09-949-016-37150	Sequence 37150, A
c 26	83.6	5.8	601	4 US-09-949-016-37163	Sequence 37163, A
c 27	83.6	5.8	601	4 US-09-949-016-37164	Sequence 37164, A

ALIGNMENTS									
RESULT 1									
US-09-360-186-1									
; Sequence 1, Application US/09360186									
; Patent No. 626243									
GENERAL INFORMATION:									
; APPLICANT: Stabakowicz, et al.									
; TITLE OF INVENTION: Bs2 Resistance Gene									
; FILE REFERENCE: 50687									
; CURRENT APPLICATION NUMBER: US/09/360,186									
; CURRENT FILING DATE: 1998-07-23									
; EARLIER APPLICATION NUMBER: 60/093,957									
; NUMBER OF SEQ ID NOS: 9									
; SOFTWARE: PatentIn Ver. 2.0									
; SEQ ID NO: 1									
; LENGTH: 31491									
; TYPE: DNA									
; ORGANISM: Capsicum annuum									
US-09-360-186-1									
Query	Match	7.9*	Score 113.8;	DB 3;	Length 31491;				
Matches	210;	Conservative	59.5*	Pred. No. 2.9e-14;	Mismatches 142;	Indels 1;	Gaps 1;		
Qy	38	CTTGATATGTTAGATTTCAGATTGCTATGAGTACGGCTGCAG 97							
Db	22086	CTCAGTTCTCTCCGAACTCGGCATAGGATCATGGCTTGTGAC 22145							
Qy	98	AGGATCCCAAAATTACTCTAAATTATCAGTCAGTCTGGAAAC 157							
Db	22146	TCG-TCTTAATGTTTCACTTCCTCATGCTTATGACAACTTGGCCATACAA 22204							
Qy	158	CCGTGGCTCACCAACTCAGTCAGTCAATATAACAGAGTATGACACTTGGAGC 217							
Db	22205	CTGACTCTCACCCACTCATACCTTCATGGACCTATTCCTCAATCAAAGC 22264							
Qy	218	CTCGTAAGGTGGCCATCTAGATGCCAGTGAACCTGTTAGCTGAGCTAAC 277							
Db	22265	CTCAAAGGAGCCATCTGTGTCGGCATGGTAACTCCATGCCCTAACATATCTC 22324							
Qy	278	CGGTAAAAATCCCTCAACTCTAGATAATCATGGCTCAATCTGATCC 337							
Db	22325	TGGAGGTGATCTACCTTGTAACTTCCATGGTAACTCCATGCCCTAACATATCTC 22384							
Qy	338	TAGTATGTAATGATCCACCTTCCTCAATTGACATCCGTTCTGAGGATGAAATCAG 390							
Db	22385	GAGGSTCTGTGATGGCTCAGGETGTCAGCTTCGGTTGTCCATCCTGAGGGTGAACCTG 22437							

RESULT 2

US-09-864-680A-1
i Sequence 1, Application US/098864680A
i Patent No. 6762285
i GENERAL INFORMATION:
i APPLICANT: Staszkowicz, Brian J
i APPLICANT: Dahlbeck, Douglas B
i APPLICANT: Tai, Thomas H
i TITLE OF INVENTION: B82 RESISTANCE GENE
i FILE REFERENCE: 42250/NUMBER: 1 (5830-4A)
i CURRENT FILING DATE: 2001-05-24
i PRIOR APPLICATION NUMBER: US/09/664,680A
i PRIOR FILING DATE: 1998-07-23
i NUMBER OF SEQ ID NOS: 14
i SOFTWARE: PatentIn version 3.1
i SEQ ID NO: 1
i LENGTH: 31491
i TYPE: DNA
i ORGANISM: Capsicum annuum
i US-09-864-680A-1

Query Match 7.9%; Score 113.8; DB 4; Length 31491;
 Best Local Similarity 59.5%; Pred. No. 2.9e-14;
 Matches 210; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

QY 38 CTTGATATCTATGATTTCGAGATTGCGATAAGACITCATCTATCAGAAAGACGCCCTGGAG 97
 •Db 22086 CTCPAGTCTCTCTCCGAAACATCGGATAGCACCTAACGACTTGGCAGCTTGAC 22145

QY 98 AGGATCCAAATTAGTCTAAATATTCTCACTTCACTGGAAACCACTCAGGACCCAAC 157
 ..Db 22146 TCG-TCTCTATGATTTCGACTTCTCACTTCATCGCCCTATGAAACAGATTGGCCATCAA 22204

QY 158 CGGTGCGTCACCCAACTCACTCTTAATATAACAGAGTATGACACTTGGACCATAGGCC 217
 Db 22205 CTGACTCTACCCACTCTACCACTTCAACATCTATGGAGACCTATATCCTCAATAAGC 22264

QY 218 CTCGTAGGTGGCCATCTAGATGCCAGATTCGAAACTGTTATTCTGAGGGAAACTCAACTAA 277
 Db 22265 CTCAAAGGAGCCATCTGTGCTGCGATGTAGTTATTCTGAAAGGAAATTGACCRG 22324

QY 278 CGGTAAAAAAATCCTCTCAACTACCTTGTATAATACATAGTCCTCAATCTGTATCTC 337
 Db 22325 TGGCAGGGTGAATCTACCAACTACCTTGTAAATCAATTACGCATGCCCTAAACATATCTC 22384

QY 338 TAGTATGATCACTTCGAAATTGACCATGCTGGGTGAGAATGCGAG 390
 Db 22385 GAGGGTCTGATGGTAGCTGAGCTGGCTAGCTGTCATCGCTGAGGGTGGAAACCTG 22437

RESULT 4
 US-09-902-540-1357/c
i Sequence 1357, Application US/09949016
i Patent No. 612339
i GENERAL INFORMATION:
i APPLICANT: Goldman, Barry S.
i APPLICANT: Hinkle, Gregory J.
i APPLICANT: Slater, Steven C.
i APPLICANT: Wiesand, Roger C.
i TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
i FILE REFERENCE: 38-10(115B)B
i CURRENT FILING DATE: 2001-07-10
i PRIOR APPLICATION NUMBER: US/09/902,540
i PRIOR FILING DATE: 2000-07-10
i NUMBER OF SEQ ID NOS: 16825
i SEQ ID NO: 1357
i LENGTH: 612
i TYPE: DNA
i ORGANISM: Myxococcus xanthus
i FEATURE:

RESULT 3
 US-09-902-540-1357/c
i Sequence 1357, Application US/09949016
i Patent No. 6833447
i GENERAL INFORMATION:
i APPLICANT: Venter, J. Craig et al.
i TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
i FILE REFERENCE: CL001307
i CURRENT FILING DATE: 2000-04-14
i PRIORITY: 1999-04-14
i PRIORITY NUMBER: 60/1239
i PRIORITY FILING DATE: 2000-04-10
i PRIORITY NUMBER: 60/241,755
i PRIORITY FILING DATE: 2000-04-20
i PRIORITY NUMBER: 60/237,768
i PRIORITY FILING DATE: 2000-10-03
i PRIORITY NUMBER: 60/231,498
i PRIORITY FILING DATE: 2000-09-08
i NUMBER OF SEQ ID NOS: 20012
i SOFTWARE: FastSEQ for Windows Version 4.0
i SEQ ID NO: 1354
i LENGTH: 59519
i TYPE: DNA
i ORGANISM: Human
i FEATURE:

SOFTWARE: PatentIn Release #1.0, Version #1.25
 APPLICATION NUMBER: US/08/487,826B
 FILING DATE: 10-SEP-1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelson, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CP1
 TELEPHONE: (619) 235-8550
 TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19124 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-487-826B-13

Query Match 6.2%; Score 88.4; DB 2; Length 19124;
 Best Local Similarity 49.8%; Pred. No. 5.2e-09;
 Matches 289; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

*Db 15951 TTTCATTTAATTAAATTTTATTGATGACCAAGTGCTACCGATGGT 488
 Qy 429 TTATTATTTAAATAATTGATGACCAAGTGCTACCGATGGT 488
 *Db 15892 CAAAGTGCCACCAATTTTTATTGATCTACCTCCTGCCTAGATTGCAATTGCAATT 548
 Qy 489 CAAGTGCCACCAATTTTTATTGATCTACCTCCTGCCTAGATTGCAATTGCAATT 548
 *Db 15832 TTATTAAATTAAATTTTTATTGATCTACCTCCTGCCTAGATTGCAATT 548
 Qy 549 TCTCATTTCAATTCAATTCAATTCAATTCAATTCAATTCAACTTTA 608
 *Db 15831 TTATTTTTTAAATAAAATTAAATTCAACTTTA---TTA 15776
 Qy 609 CTTTTTTAAAGAAATTATTAAATTATTAAATTCTAAATAC 668
 *Db 15775 ACATTTTAAATTTTTATTGATATTATTTTCTCTTC 15716
 Qy 669 TTACTTTTTAAAGAAATTCAATTGCTTTCTCAATTGATTTA 728
 *Db 15715 TTGTGTTTTGTGTTTTGTGATATAATTGTTTCTCTCT 15656
 Qy 729 TACTAAATTAAATTCTGATCGGATTTAGTGCTGGTCAAGTCACAGAAATT 788
 *Db 15655 TTGTGTTTTGTGTTTTGTGATATAATTGTTTCTCTCT 15596
 Qy 789 TGTGAGAGAAAAATAAAATTAAACACATTTCGATTAATTATTATAATAA 848
 *Db 15595 TTGATPAATCTTTTCATTTTATTCTCATGAAATTATTATA 15536
 Qy 849 TATAAACACATTTTATTAAATTGATGTCATAATTATTAAATTTCAGCAAA 908
 *Db 15535 TTTTAAAAATTCTCCTTTTTTTTTTTTTTTTTTTTTTTT 15486
 Qy 909 CAATTACACTCTCATATAATTAAATTCTACCATATAAAATTGTGAGCAAT 968
 *Db 15485 -AAATTTTTTATTCTCATTTTATTCTCATTTTATTCTCATTTTATT 15427
 Qy 969 TATTTTTAATCTCACCTCCATTAAATGCCATTATTAAAT 1008
 *Db 15426 TCTTTTTAATATAACATATAATTATAAAATATAAT 15387

Query Match 6.2%; Score 88.4; DB 4; Length 205044;
 Best Local Similarity 49.1%; Pred. No. 9.2e-09;
 Matches 288; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

Qy 427 AAATTATTTTAAATAATTGATGCTACCGATGGTCTACCGATGG 486
 *Db 201233 ARCAAAATTATTGTAATCTGCTTATTCTCTGAAAGGATTTAGAGAAACAC 201174
 Qy 487 GTCTGCGCACCATTATTATTACCTCCGCTAGATTGCTAACTATGCAATT 546
 *Db 201173 TTCTGTGTTCATAGATGGGTCAATTCTCATTTAAATTCAAAATTATAATT 201114
 Qy 547 TATCTCATTCATTATTATTATTATTATTATTATTGATTAATTCTATAACTT 606
 *Db 201113 TATTTAAATAATAATTATAATTATAATTATAATTATAATTATAATT 201054
 Qy 607 TACTTTTTAAAGAAATTATTAAATTATTATAATTGATTTAAATTCTAAAT 666
 *Db 201053 TATTTTAAATTAAATTATAATTATAATTATAATTATAATTATAATT 200994
 Qy 667 ACTTACATTTTTAAAGAA ATTCAATTGCGTTTTCTCAATTGTTTANT 725
 *Db 200993 TATTTTAAATTAAATTATAATTATAATTATAATTATAATTATAATT 200934
 Qy 726 CTATCAATTAAAATTCTGATGGATTAGTGCTGTCAAGTCATGAA 785
 *Db 200933 TTATTTAAATTATAATTATAATTATAATTATAATTATAATTATAATT 200874
 Qy 786 TTCTGTTGGAGAAAAAAATTAAACACATTTCGATTATTATTATAATTATAA 845
 *Db 200873 TTATTTAAATTATAATTATAATTATAATTATAATTATAATTATAATT 200815
 Qy 846 TAATATAACACATTTTATTATTATTATTATTATTATTATTATTATT 905
 *Db 200814 ATATTTTTATATTATAATTATAATTATAATTATAATTATAATT 200755
 Qy 906 CAACATTACACTCTCATATAATTCTACCATATAAAATTGTGAGGAC 965
 *Db 200754 ATATATAAAATTATTATTATTATTATTATTATTATTATTATTATT 200695
 Qy 966 ATATTTTTAAACTCTCACCCTCCATTAAATGCCATTATTAAATT 1011
 *Db 200694 ATTATTTAAATAAAATATAAAATATAAAATATAATTATAATT 200649

RESULT 7
 US-09-949-016-15851/C
 ; Sequence 15851, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:

RESULT 8
 US-09-949-016-15852/C
 ; Sequence 15852, Application US/09949016
 ; Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIORITY NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 15852
 LENGTH: 205044
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) ..(205044)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-15852

Query Match 6.2%; Score 88.4; DB 4; Length 205044;
 Best Local Similarity 49.1%; Pred. No. 9.2e-09;
 Matches 288; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

Qy 427 AATTATTATTTTAAAATGTGTAACCGAGTGGAGAGGGTCTACGGATG 486
 Db 201233 AACAAATTATTGTAAATCTGACTTATCCTGAAANGGGATTAGACAACAC 201174

Qy 487 GTCAAGTGGCACCAATTTCATTATCCCTCTGCATGATTCTGCAATTGCAATT 546
 Db 201173 TTCACTTCATAGTAGGGTCAATTCTCATTTAAATATTCATAATTATT 201114

Qy 547 TATCTCATTCATTATTATTAAATTATTATATTATTTGATAAAATTCTATACTT 606
 Db 201113 TATATTAAAATATAAATATATATATATTTATATTTATATTTA 201054

Qy 607 TACTTTTTTAAAAGAAATTATTATTATTATTTATTTATATTTATTTA 666
 Db 201053 TATATTATTTAAATATAAATATTTATATTTATATTTATATTTA 200994

Qy 667 ACTTACTTTTTTAAAGA - ATTCAATTGGTTCTCAATTAGTTTAATT 725
 Db 200993 TATATATTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 200934

Qy 726 CTATACATTATAAAAATTCTGATGGATTAGTGTTCAAGTCAGTCAATGAA 785
 Db 200933 TTATATATTATTTAAATATAATATTTATTTATTTATTTATTTA 200874

Qy 786 TTGGTGGAGAAAAATAAAATTAACACATTTCGATTAATTATTTATAA 845
 Db 200873 TTATATATTATTTAAATATAATTTATTTATTTATTTATTTA 200815

Qy 846 TAATATAAACATTTTATTAATTTGTAATTAATTAAATTTCAGCA 905
 Db 200814 ATATTTTATTTATTTATTTATTTATTTATTTATTTATTTA 200755

Qy 906 CAACAAATTACACTCTCATCAATTAAATTCTTAACTATAAATTGTGAGGAC 965
 Db 200754 ATATATAAACATTTTATTTATTTATTTATTTATTTATTTATTTA 200695

Qy 966 AATTATTTTTAATCTCACCCCTCCATTAAATGCAATTATTTATTTT 1011
 Db 200694 ATTATTTAAATATAAATATAATTTATTTATTTATTTATTTA 200649

; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949, 016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-02
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 15853
 ; LENGTH: 205044
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) ..(205044)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-15853

Query Match 6.2%; Score 88.4; DB 4; Length 205044;
 Best Local Similarity 49.1%; Pred. No. 9.2e-09;
 Matches 288; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

Qy 427 AATTATTATTTTAAAATGTGTAACCGAGTGGAGAGGGTCTACGGATG 486
 Db 201233 AACAAATTATTGTAAATCTGACTTATCCTCTGAANGGGATTAGACAACAC 201174

Qy 487 GTCAAGTGGCACCAATTTCATTATCCCTCTGCATGATTCTGCAATTGCAATT 546
 Db 201173 TTCACTTCATAGTAGGGTCAATTCTCATTTAAATATTCATAATTATT 201114

Qy 547 TATCTCATTCATTATTATTAAATTATTATTTGATAAAATTCTATACTT 606
 Db 201113 TATATTAAAATATAAATATTTATTTATTTATTTATTTA 201054

Qy 607 TACTTTTTTAAAAGAAATTATTATTATTATTTATTTATTTATTTA 666
 Db 201053 TATATTATTTAAATATAAATTTATTTATTTATTTATTTA 200994

Qy 667 ACTTACTTTTTTAAAGA - ATTCAATTGGTTCTCAATTAGTTTAATT 725
 Db 200993 TATATATTATTTATTTATTTATTTATTTATTTATTTATTTA 200934

Qy 726 CTATACATTATAAAAATTCTGATGGATTAGTGTTCAAGTCAGTCAATGAA 785
 Db 200933 TTATATATTATTTAAATATAATTTATTTATTTATTTATTTA 200874

Qy 786 TTGGTGGAGAAAAATAAAATTAACACATTTCGATTAATTATTTATAA 845
 Db 200873 TTATATATTATTTAAATATAATTTATTTATTTATTTATTTA 200815

Qy 846 TAATATAAACATTTTATTAATTTGTAATTAATTAAATTTCAGCA 905
 Db 200814 ATATTTTATTTATTTATTTATTTATTTATTTATTTA 200755

Qy 906 CAACAAATTACACTCTCATCAATTAAATTCTTAACTATAAATTGTGAGGAC 965
 Db 200754 ATATATAAACATTTTATTTATTTATTTATTTATTTATTTA 200695

Qy 966 AATTATTTTTAATCTCACCCCTCCATTAAATGCAATTATTTATTTT 1011
 Db 200694 ATTATTTAAATATAAATATAATTTATTTATTTATTTA 200649

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Sequence 12387, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 12387
LENGTH: 223471
TYPE: DNA
ORGANISM: Human
FEATURE NAME/KEY: misc_feature
LOCATION: (1) - (223471)
OTHER INFORMATION: n = A, T, C or G
US-09-949-016-12387

Query Match Score 88.4; DB 4; Length 223471;
Best Local Similarity 49.1%; Pred. No. 9.4e-09;
Matches 288; Conservativeness 0; Mismatches 296; Indels 2; Gaps 2;
Qy 427 AATTATTATTTTAAATGATGTGACCAAGCTGGTGGAGAGGGTCTACGGATTG 486
Db 171650 AACAAATTATTGTAACTCTGACTTATTCTCTGAAGGGATTAGAGAACAC 171601
Qy 487 GTCAAGTGGCACCATTTCATTTACCTCCCTCGCTAGATTCGTAATACTATGCAATT 546
Db 171650 TTCTATGTTCATAGAGGGTCATTCCTCAATTAAATAATTCAAAATAATATT 171541
Qy 547 TATCTCATTCATTTATTATTAAATTATTTATTTATTTATGATAAAAATTCTAACTCT 606
Db 171540 TATATTAAATATATAATATATTTATTTATTTATTTATTTATTTATTTA 171481
Qy 607 TACUTTTTTAAAGAATTATTAAATTATTTATTTATTTATTTATTTATTTATTTA 666
Db 171480 TATTTATTTATTTAAATATATTTATTTATTTATTTATTTATTTATTTA 171421
Qy 667 ACUTTACTTTTTAAAGA-ATTCTGATTGGTTTCTTAATTAGTTTAAATT 725
Db 171420 TATTTATTTATTTAAATATATTTATTTATTTATTTATTTATTTATTTA 171361
Qy 726 CTACTACTATTATAAAATTCTGATGGATTAGTCGTGCTCAAGTCAGTCATGAA 785
Db 171360 TTTTATTTATTTATTTAAATATTTATTTATTTATTTATTTATTTATTTA 171301
Qy 786 TTGTTGAGAAAAAAATAAACATTTTGATTTGATTTATTTATTTATTTATTTA 845
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Qy 966 AATTATTTTAATCTCACCTCCATTAAATGCTATTGATTTATTTATTTATTT 1011
Db 171121 ATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 171076

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US-09-949-016-12724/c
Sequence 12724, Application US/0949016
; Sequence 12724, Application US/0949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASES
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIORITY NUMBER: 60/237,768
; PRIORITY NUMBER: 60/231,498
; PRIORITY NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ For Windows Version
; SEQ ID NO: 12724
; LENGTH: 23471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724

Query Match          6.2% ; Score 8
Best Local Similarity 49.1% ; Pred. N
Matches 238; Conservative 0; Mismatch
Db 171660 AACAAATTATTGTAACTGACTTAA

QY 427 AATTATTATTTAAAAAATTGATTC
QY 487 GTCAAGTGGCACCATTTTATTATA
Db 171600 TTCTATGTTATGATAGGGTCAATT

QY 547 TATCTCATTCATTATTAACTTAATA
Db 171540 TATATTAATAATATAAATATTTT
QY 607 TACTTTTTTAAAGAAATTATTA
Db 171480 TATATTAATTTAAATATATATT
QY 667 ACTTACTTTTTTAAAGAA-ATT
Db 171420 TATATTTATTTAAATATATAA

QY 726 CTATACAAATTAAATTCGTGCC
Db 171360 TTATPATATTATAATTAATATA
QY 786 TTGTGTGGAAAAATAAAATTAATTA
Db 171300 TTITTTATTTATTTAAATATAAATTA

QY 846 TAATATAAACATTTATTAATATG
Db 171241 ATATTTATATTTATTTAAATTAAT
QY 906 CAACAAATTACACTCTCATCATAAAAT
Db 171181 AAATATATAATATTTATATAATTA

QY 966 ATTATTTTTAATCTCACCCTCCATT
Db 171121 ATTTPATTTAAATATAATTAATTAAT

```

RESULT 12
US-09-949-016-12725/c
Sequence 12725; Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIORITY NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 12725
LENGTH: 223471
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(223471)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725

Query Match Score 6.2%; DB 4; Length 223471;
Best Local Similarity 49.1%; Pred. No. 9.4e-09;
Matches 288; Conservative 0; Mismatches 296; Indels 2; Gaps 2;

Qy 427 AATTATTATTTTAaaaaATTGATGAGCAACGGTGTGGAGAGGCTACGATTG 486
Db 171660 AACAAATTTTATTGTAATTCTGACTTTATTCTCCCTGAAACGGATTAGAGACAAC 171601
Qy 487 GTCAAGTGGCACCAATTTTATTACCTCCTGCCTAGATTGTAATCTATGCAATT 546
Db 171600 TCTATGTTTCATAGATGGGTCAATTCTGATTAATTATTATATTATTATT 171541
Qy 547 TATCTCTATTCAATTATTAAATTATTATTATTATTATTATTATTATTATTATTATT 606
Db 171540 TATATTTAAATATAATTATATTATATTATATTATATTATATTATTTA 171481
Qy 607 TACTTTTTAAAAAGAAATTATTAAATTATTATTATTATTATTATTATTATTATT 666
Db 171480 TATATTATTATTTAAATTATTATTATTATTATTATTATTATTATTATTATTATT 171421
Qy 667 ACTTTACTTTTTTTAAAAAGA -ATTCAATTGCCTTTCTPATTTAGTTTAATT 725
Db 171420 TATATTATTATTTAAATTATTATTATTATTATTATTATTATTATTATTATT 171361
Qy 726 CTATACATTAAATTCTGATCGGATTAGTGCTGCAACTCAAGTCAGTCAA 785
Db 171360 TTATATATTATTAAATTATTATTATTATTATTATTATTATTATTATTATTATT 171301
Qy 786 TTGTGTTGAGAAAATTAAACATTTTGATTAATTATTATTATTATTATTATAA 845
Db 171300 TTTTTATATTATTATTAAAA-TATATTATTATTATTATTATTATTATTATT 171242
Qy 846 TAATATAAAACATTTTTATTAAATGTGTCAATAATTTTTAATTAAATTICAGCA 905
Db 171241 ATATTATTATTTATTATTAAATTATTATTATTATTATTATTATTATTATAA 171182
Qy 906 CAACAAATTACACTCTCATCAATTAAATTCTTACCTTAATTAACTTACATTGAGAC 965
Db 171181 ATATATAAAATTATTAAATTATTAAATTATTATTATTATTATTATTATT 171122
Qy 966 ATTATTATTTTAACTCTGACCCCTCAATTCTTAAATTGTGAGATAATTATT 1011
Db 171121 ATTATATAAAATTATTAAATTATTAAATTATTATTATTATTATTATTATT 171076

RESULT 13
US-09-949-016-17369
Sequence 17369; Application US/09949016
Patent No. 612339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIORITY NUMBER: 60/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 17369
LENGTH: 61178
TYPE: DNA
ORGANISM: Human
US-09-949-016-17369

Query Match Score 6.1%; DB 4; Length 61178;
Best Local Similarity 49.9%; Pred. No. 1.1e-08;
Matches 275; Conservative 0; Mismatches 271; Indels 5; Gaps 2;

Qy 546 TTATCTCATTCATTATTATTATTATTATTATTATTATTATTATTATTCTAAACTCTAA 605
Db 21250 TAATCTCATTCATTATTATTATTATTATTATTATTATTATTATTCTTATATTATTATT 21309
Qy 606 TTACTTTTTAAAAAGAAATTATTAAATTATTATTATTATTATTATTATTATTATT 665
Db 21310 ATAATCTCATTCATTATTATTATTATTATTATTATTATTATTATTATTATTATAAA 21369
Qy 666 TACTTACATTTTTTAAAAAGAAATTCAATTGGCTTTTCTTAATTAGTTTAATT 725
Db 21370 TCTATATCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 21429
Qy 726 CTATACATTATTAAATTCTGATCGGATTAGTGCTGTCAAAGTCAGTCAGTCAA 785
Db 21430 ATAATCTTATTATTAAATTATTATTATTATTATTATTATTATTATTATTATTATT 21488
Qy 786 TTGTGTTGAGAAAATTAAACATTTTGATTAATTATTATTATTATTATTATAA 845
Db 21489 ATAATCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAA 21548
Qy 846 TAATATAAAACATTTTTATTAAATGTGTCAATTATTATTATTATTATTATTATAA 905
Db 21549 TTATATATTATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAA 21608
Qy 906 CAACAAATTACACTCTCATCAATTAACTTACATTAACTTACATTAACTTACATT 961
Db 21609 TATATATATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATAA 21668
Qy 962 GGACATTATTATTATTAACTCTACCCCTCAATTATTGATTAATTATTATAA 1021
Db 21669 ATATATCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATAA 21728
Qy 1022 TTCTTATTCACTCTCATCAATTAACTTACATTAACTTACATTAACTTACATT 1081
Db 21729 TCTATCTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 21788
Qy 1082 CTTATTCACTA 1.092
Db 21789 ATTATATAAA 21799

RESULT 14
US-09-949-016-12776/c

Sequence 12776, Application US/09949016
 Patent No. 6812339

GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CL001307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241, 755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237, 768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231, 498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 12776
 LENGTH: 187169
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(187169)
 OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12776

Query Match 6.0%; Score 85.8; DB 4; Length 187169;
 Best Local Similarity 51.0%; Pred. No. 3.1e-08;
 Matches 281; Conservative 0; Mismatches 262; Indels 8; Gaps 3;

Qy 538 TATTGGATTTATCTCATTTCAATTATTAAATTATTTATATAT-TTGGATAAAAAT 596
 . Db 1036 TATTATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 977

Qy 597 TCTTAATCTTACTTTTAAAGAAATTATTTATTTATTTATTTAGATAA 656
 Db 976 TATATATCCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 917

Qy 657 AAATTCTAATCTTACTTTTAAAGAAATTCAATTGGCTTTTCCTTAATTAA 716
 Db 916 TATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 857

Qy 717 GTTTAAATCTCATTTATTTATTTATTTATTTATTTATTTATTTATTTA 803
 Db 856 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 803

Qy 777 TCACATGAAATTGTGGAGAAAAATAAAACATTTTCGATTAATTATAA 836
 Db 802 TTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 743

Qy 837 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 896
 Db 742 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 683

Qy 897 ATTCAGCACACAATTACACTCTCATCATTAATTAACTTATCCATAATTAAAT 956
 Db 682 TATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 623

Qy 957 TGTGAGGACAAATTATTTTAATCTCACCCTCAATTATGATTTAT-TAATTGTTGTT 1015
 Db 622 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 563

Qy 1016 CGATACTCTTATTCTCATCTCTAACATTAACCCRAATTGAACTGTATAATT 1075
 Db 562 TTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 503

Qy 1076 TCTTAACTTAT 1086
 Db 502 ATATTTTTAT 492

US-09-949-016-15940

Query Match 6.0%; Score 85.8; DB 4; Length 191569;
 Best Local Similarity 51.0%; Pred. No. 3.2e-08;
 Matches 281; Conservative 0; Mismatches 262; Indels 8; Gaps 3;

Qy 538 TATTGCATTTCTCATTTCAATTATTAAATTATTTATTTATTTATTTATTTAAT 596
 . Db 1036 TATTATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 977

Qy 597 TCTTAATCTTACTTTTAAAGAAATTATTTATTTATTTATTTATTTAGATAA 656
 Db 976 TATATATCCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 917

Qy 657 AAATCTAATCTTACTTTTAAAGAAATTCAATTGGCTTTTCCTTAATTAA 716
 Db 916 TATATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 857

Qy 717 GTTTAACTTACTTTATTTATTTATTTATTTATTTATTTATTTATTTA 803
 Db 856 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 803

Qy 777 TCACATGAAATTGTGGAGAAAAATAAAACATTTTCGATTAATTATAA 836
 Db 802 TTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 743

Qy 837 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 896
 Db 742 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 683

Qy 897 ATTCAGCACACAATTACACTCTCATCATTAATTAACTTATCCATAATTAAAT 956
 Db 682 TATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 623

Qy 957 TGTGAGGACAAATTATTTTAATCTCACCCTCAATTATGATTTAT-TAATTGTTGTT 1015
 Db 622 TATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 563

Qy 1016 CGATACTCTTATTCTCATCTCTAACATTAACCCRAATTGAACTGTATAATT 1075
 Db 562 TTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTA 503

Qy 1076 TCTTAACTTAT 1086
 Db 502 ATATTTTTAT 492

Search completed: August 13, 2005, 13:15:41
Job time : 623 secs

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Result No.	Score	Query	Match Length	DB ID	Description
C 1	137.8	9.6	4950	20 US-10-425-115-109152	Sequence 109152,
C 2	136.4	9.5	4977	20 US-10-425-115-109152	Sequence 109152,
C 3	133.6	9.3	4623	20 US-10-425-115-109144	Sequence 109144,
C 4	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 5	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 6	131.1	9.1	4064	20 US-10-425-115-109142	Sequence 109142,
C 7	129.4	9.0	2460	20 US-10-425-115-162914	Sequence 162914,

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description	
C 1	137.8	9.6	4950	20 US-10-425-115-109152	Sequence 109152,
C 2	136.4	9.5	4977	20 US-10-425-115-109152	Sequence 109152,
C 3	133.6	9.3	4623	20 US-10-425-115-109144	Sequence 109144,
C 4	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 5	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 6	131.1	9.1	4064	20 US-10-425-115-109142	Sequence 109142,
C 7	129.4	9.0	2460	20 US-10-425-115-162914	Sequence 162914,

RESULT 1
US-10-425-115-109152/C
/ Sequence 109152, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovacic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-215322/B
/ CURRENT APPLICATION NUMBER: US/10425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 109152
/ LENGTH: 4950
/ TYPE: DNA
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_31042C-1
US-10-425-115-109152

ALIGNMENTS

Title	Score	Match Local Similarity	Pred. No.	Mismatches	Indels	Gaps
OM nucleic - nucleic search, using sw model	9.6%	62.2%	0	0	0	0;
Run on: August 13, 2005, 11:00:09 ; Search time 8243 Seconds (without alignments)	9.0	4530	20 US-10-425-115-109139	Sequence 109139,		
Sequence: 1 actataggcacgcgtggtc.....tgagagaatcttcacatc 1433	9.0	4530	19 US-10-425-115-109139	Sequence 109139,		
Scoring table: IDENTITY_NUC GapP 10_0 , Gapext 1.0	9.0	4530	19 US-10-425-115-109139	Sequence 109139,		
Post-processing: Minimum Match 100% Maximum Match 100% Listing First 45 Summaries	9.0	4530	19 US-10-425-115-109139	Sequence 109139,		
Database : Published Applications NA: *	9.0	4530	19 US-10-425-115-109139	Sequence 109139,		
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2: /cgm2_6/podata/2/pubpna/PCT_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
3: /cgm2_6/podata/2/pubpna/us06_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
4: /cgm2_6/podata/2/pubpna/us05_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
5: /cgm2_6/podata/2/pubpna/PCTUS07_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
6: /cgm2_6/podata/2/pubpna/PCTUS08_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
7: /cgm2_6/podata/2/pubpna/us08_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
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9: /cgm2_6/podata/2/pubpna/us09A_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
10: /cgm2_6/podata/2/pubpna/us09B_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
11: /cgm2_6/podata/2/pubpna/us09C_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
12: /cgm2_6/podata/2/pubpna/us09_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
13: /cgm2_6/podata/2/pubpna/us10_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
14: /cgm2_6/podata/2/pubpna/us10C_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
15: /cgm2_6/podata/2/pubpna/us10D_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
16: /cgm2_6/podata/2/pubpna/us10E_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
17: /cgm2_6/podata/2/pubpna/us10F_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
18: /cgm2_6/podata/2/pubpna/us10G_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
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20: /cgm2_6/podata/2/pubpna/us10I_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
21: /cgm2_6/podata/2/pubpna/us10J_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
22: /cgm2_6/podata/2/pubpna/us10K_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
23: /cgm2_6/podata/2/pubpna/us11A_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
24: /cgm2_6/podata/2/pubpna/us11A_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
25: /cgm2_6/podata/2/pubpna/us60_NEW_PUB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		
26: /cgm2_6/podata/2/pubpna/us60_PUBCOMB.seq:*	8.9	4530	19 US-10-425-115-109139	Sequence 109139,		

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description	
C 1	137.8	9.6	4950	20 US-10-425-115-109152	Sequence 109152,
C 2	136.4	9.5	4977	20 US-10-425-115-109152	Sequence 109152,
C 3	133.6	9.3	4623	20 US-10-425-115-109144	Sequence 109144,
C 4	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 5	131.2	9.2	4719	20 US-10-425-115-109143	Sequence 109143,
C 6	131.1	9.1	4064	20 US-10-425-115-109142	Sequence 109142,
C 7	129.4	9.0	2460	20 US-10-425-115-162914	Sequence 162914,

Query Match 9.6%; Best Local Similarity 62.2%; Matches 217; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 58 GATTCGATAGACTCTCATATCGAAAGCCGCTGCCATTAGTCTAA 117
Db 4492 GGTCTGCATACCTCTGAGCTGGCTTCTCATATTGAAATTCTATGAA 4433

RESULT 2
 US-10-425-115-177410
i Sequence 177410, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
** i* APPLICANT: La Rosa, Thomas J.
** i* APPLICANT: Kovalic, David K.
** i* APPLICANT: Zhou, Yihua
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i Title: Plants
i FILE REFERENCE: 38-21(5322)B
i CURRENT APPLICATION NUMBER: US/10/425,115
i CURRENT FILING DATE: 2003-04-28
i NUMBER OF SEQ ID NOS: 369326
i SEQ ID NO: 109140
i LENGTH: 4977
i TYPE: DNA
i ORGANISM: Zea mays
i FEATURE:
i OTHER INFORMATION: Clone ID: MRT4577_93387C.1
 US-10-425-115-177410
i Sequence 177410, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
** i* APPLICANT: Cao, Yongwei
** i* APPLICANT: Zhou, Yihua
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i Title: Plants
i FILE REFERENCE: 38-21(5322)B
i CURRENT APPLICATION NUMBER: US/10/425,115
i CURRENT FILING DATE: 2003-04-28
i NUMBER OF SEQ ID NOS: 369326
i SEQ ID NO: 109140
i LENGTH: 4977
i TYPE: DNA
i ORGANISM: Zea mays
i FEATURE:
i OTHER INFORMATION: Clone ID: MRT4577_93387C.1
 RESULT 3
 US-10-425-115-109144/C
i Sequence 109144, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
** i* APPLICANT: La Rosa, Thomas J.
** i* APPLICANT: Kovalic, David K.
** i* APPLICANT: Zhou, Yihua
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i Title: Plants
i FILE REFERENCE: 38-21(5322)B
i CURRENT APPLICATION NUMBER: US/10/425,115
i CURRENT FILING DATE: 2003-04-28
i NUMBER OF SEQ ID NOS: 369326
i SEQ ID NO: 109144
i LENGTH: 4623
i TYPE: DNA
i ORGANISM: Zea mays
i FEATURE:
i OTHER INFORMATION: Clone ID: MRT4577_31035C.1
 US-10-425-115-109144
 Query Match 9.3%; Score 133.6; DB 20; Length 4623;
 Best Local Similarity 62.1%; Pred. No. 2e-0; Gaps 0;
 Matches 211; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
 Qy 58 GATTGCATAGAGCTTCTATCTATCATAGAGACGCTGAGAGATCCAAATTAGTCATAA
 Db 4165 GGTCGTGCATAACTCTTTTGCGAGCCTGAGCTTCTCATATGACAATTTCGTGAA
 4106 118 AATTATCTTCAGTCTGGAAACCAACTCTGGAAACCCGTCACCAACTAG 177
 Db 4105 CCTTTCTCGACCTCTTCACRATTCATGGCTTAAAGAATTCCTTCAGGTTCTGAG 4046
 Qy 178 TCTPATAATAACAGGTATGACACTTATGACCATATAGCCATTCCTTAAGTGCCATCTAGA
 Db 4045 ACCATTAGGGAGTCAGCTGGAAACCCGTCACCAACTAG 177
 Db 238 TGCAGATGGAAACCTGTATTGTAGGGAAACTAACCTGAAATTCCTTCACAC 297
 Db 3985 TACTTCTGATAACTGTTATGTGAAAACCTCGGTAGGGCAAAATTCCTCCATT 3926
 Qy 298 TACCTTAGATAATACTACATGGCTCAAATGGTATGATAAGTTAAAGCTTAAAGCTGA
 Db 3925 TTGGTGAAGAATTCAGGACACACGCCGATATCTCAAGTTGTTCCCCTCT 3866
 Qy 358 CAAATTGACCATCGGTCTGGAGTGAATGCAAGCCGGTGTG 397
 Db 3865 CAGTGTCCACCTGGTTAGGATGATAAGCGAACTGTG 3826
 RESULT 4
 US-10-425-115-109143/C
i Sequence 109143, Application US/10425115
i Publication No. US20040214272A1
i GENERAL INFORMATION:
** i* APPLICANT: La Rosa, Thomas J.
** i* APPLICANT: Kovalic, David K.
** i* APPLICANT: Zhou, Yihua
i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
i Title: Plants
i FILE REFERENCE: 38-21(5322)B
i CURRENT APPLICATION NUMBER: US/10/425,115
i CURRENT FILING DATE: 2003-04-28
i NUMBER OF SEQ ID NOS: 369326
i SEQ ID NO: 109143
i LENGTH: 4719
i TYPE: DNA
i ORGANISM: Zea mays
i FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_31034C.1
US-10-425-115-109143

Query Match 9.2%; Score 132; DB 20; Length 4719;
Best Local Similarity 61.8%; Pred. No. 3.4e-09;
Matches 210; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
Seq ID NO: 23515; Application US/10437963

Qy 58 GATTTGCAATAAGACTCTATCAGAAGACGCTGAGGATCCAAATTAGTCAA 117
Db 4261 GGTCCTGCAATAACTCTTGTGAGTCAGCTTGCTCATATGAAATACTCTGAA 4202
Qy 118 AATTATCTTCAGTCTCGGAACCAACTCAGGACCCAAACCCGTCGCTCACCAACTCAG 177
Db 4201 CCTTTCTTGACCTCTTACCATATCAGGCCCTAAAGAAGTACTTCTCCAGGTTAG 4142
Qy 178 TCTTAATATAACAGACTGACACTATGACCATAAGGGCTGTAAGTGCATCTAGA 237
Db 4141 ACCAATTACGGACTTGCACCTGCGTCCATTAAGCTTCAAAGGTGCCATCTGA 4082
Qy 238 TGCCAGATTTGGAAACTCTGTTATTGAGGGAAACTAACGTTAAATCCCTCAC 297
Db 4081 TACTTCTGATAACTGTTATTGAGAAATTCCGTTAGGGAAACCATCATCCATT 4022
Qy 298 TACCTTAGTAAATAATCACATAGCTCCAATCTGTTCTAGTATGAAATCACCTCT 357
Db 4021 TTGGCGAAAGTCCAGAACATGCCCGACGATATCCCTGAGTATCTCT 3962
Qy 358 CAAATTGACCATGCTGGTCAAGGATGAAATCGACGGGCG 397
Db 3961 CAGTCTGTCACACTGGTTGAGGATGATGCCGAACTGTC 3922

RESULT 5
US-10-437-963-23515/C

; Sequence 23515, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbak, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_2858BC.1
US-10-437-963-23515

Query Match 9.2%; Score 131.2; DB 19; Length 3285;
Best Local Similarity 61.3%; Pred. No. 4e-09;
Matches 211; Conservative 0; Mismatches 133; Indels 0; Gaps 0;
Seq ID NO: 23515; Application US/10437963

Qy 52 TTTTCAGATTGCAATAAGACTCTATCATATGAAAGACGCTGAGGATCCAAATTA 111
Db 1953 TTCTGACATCGCCGTAAGCTCTCTGCTACTTGTACCCGAGAATGTGTGCCCTATCT 1894
Qy 112 GTCTAAATATCTTCTAGTCGGAAACCAACTCAGGCCAAACCGTGTGCTACCCA 171
Db 1893 CTGCTATCGTGTCTGTCAGCTGCTGGTCAACCTCTCCTAAATAGCTCTCCTA 1834
Qy 172 ACTCACTCTAAATAACAGAGTATGACACTPATGACCATATAGAGCTCGTAAGGTGCCA 231

1833 TGGATCCAAACACAATGGGATGCACTTCTCCATACAGTGCCTCATATGGTGCCTA 1774

232 TCTPAGATGCCAGATTGGAAACCTGTTATGAGGGAAACTCAACTAACGTTAAAATCTC 291
1773 TTCCAAATGTTGAGCTGTTGAACTATGTTGAGGAAATCTACGGGCCAAATGATCTC 1714
292 CTCACACTCTTGTAAATTCAGTCATAGCTCAAAATGTTCTACTATATGAACTCA 351.
1713 CCCACTGCCTTCATGAAATTACATGATCTAACATCTAGGTTGAATGATCG 1654

Qy 352 CCTTCTCAATTGCCATGGTCTGAGGATGGAGACCCG 395
Db 1653 TCCGCTCAGATTGCCATGAGCTGAGGTGAAAGGCCCTACTCG 1610

RESULT 6

US-10-435-115-177422
; Sequence 177422, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plant
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 363326
; SEQ ID NO: 177422
; LENGTH: 4064
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93398C.1
US-10-425-115-177422

Query Match 9.1%; Score 131; DB 20; Length 4064;
Best Local Similarity 61.1%; Pred. No. 4.5e-09;
Matches 212; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 60 TTTCGATAAGACTCTATCTATCATAGAAAGACGCTGAGGATCCAAATTAGCTAA 119
Db 461 TCTGCTAAACTCTTGGCGTGTGCTGAGCTTCTCATATTATGATAATTCTGAAAC 520
Query Match 9.1%; Score 131; DB 20; Length 4064;
Best Local Similarity 61.1%; Pred. No. 4.5e-09;
Matches 212; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 120 TTATCTTCAGTCGGAAACCAAATCAGGACCCAAACCGTCTCACCCAACTCAGTC 179
Db 521 TTTCCTTCACCTCTTCCACCATATCAGCTCTAAAGAAAGTATCTTCAGGTCA 580
Qy 180 TAATAAACAGAGPATGACACTTATGACCATATGAGCTCTGTAAGGTGCCATCTGATA 239
Db 581 CAATTAGGGAGTCGAGACCCGAGTCGAGCTCTTAAAGCTCAAGGTGCACTTGTATA 640
Qy 240 CCAGTTGGAAACTTTATGAGCTGCAACTCAACTAACCGTAAAAATCTCTCAACTA 299
Db 641 CCTTCCTGGPATGACATTATATGAAACTCCATCCATTIT 700

Qy 300 CCTTGTAAATAATACATAGCTCCAATGTTCTCTAGTATGAAATCACCTCTCTCA 359
Db 701 AGTGAAATCCAGAACATGCGCAGCATATCTCAAGTATTGGTCACTCTCTCA 760
Qy 360 AATGACCATGGTTGAGATGGAAATGAGACCCGGTGCACCGATT 406
Db 761 GTRIGTCACCTGGTTGAGATGGAAATGAGACCCGGTGCACCGATT 807

RESULT 7

US-10-425-115-162914/C
; Sequence 162914, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 162914
 LENGTH: 2460
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_80152C.1
 US-10-425-115-162914

Query Match 9.0%; Score 129.4; DB 20; Length 2460;
 Best Local Similarity 61.4%; Pred. No. 6.6e-09;
 Matches 208; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy 59 ATTTGCGATAAGACTCTATCATAGAAGACGGCTGAGAGGATCCAAATTAGTCATAA 118
 Db 2001 ATTCGCGTAACCTCTCTGAGGCTTCTTCATAAATTGAAATTCTGTGAAAC 1942

Qy 119 ATTATCTAGTCTCGGAAACCAACTAGAACCCGCTCACCAACTCTGAT 178
 Db 1941 CCTTCCTCTGCTCCTTACCATATCGGCCCTGAAGAAATATCTTACCGAGTTCTGA 1882

* Qy 179 CTAATATACAGAGTATGACACTATGACCATAATAGAGCTCGTAAGGTGCCATCTGAT 238
 Db 1881 CCAGTTAACGGAGTCAAACATGTCGTCCATAAAAGTTCTGAGGGTGCATCTTAT 1822

* Qy 239 GCCAGATGGAAACTGTATTGTAGGGAACTCAACTAACGGTAAAAAATCCTCTCACT 298
 Db 1821 ACTTCTGTAGCTATTATATGAGAACATCCGCTTAATGTTAACATCCATT 1762

Qy 299 ACCCTAGTAATAATCACATAGCTCAAATGTPATCTCTAGATATGATCACCTCTC 358
 Db 1761 CTGTCGGAACTCCAGAACACATGCTCGAACATCTGAGPATCTGTTAACCTCTC 1702

Qy 359 AAATTGACCATCGGCTGAGGATGAAATGAGACGGGTG 397
 Db 1701 AGTCGCCACTGGTTGAGGATGAGCTGGCAACTATG 1663

RESULT 8
 US-10-425-115-109139/c
 Sequence 109139, Application US/10425115
 Publication No. US20040214272A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(53222)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 369326
 SEQ ID NO: 109139
 LENGTH: 4530
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: MRT4577_31030C.1
 US-10-425-115-109139

Query Match 9.0%; Score 129.4; DB 20; Length 4530;
 Best Local Similarity 60.8%; Pred. No. 7.7e-09;
 Matches 211; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy 60 TTTGCGATAAGACTCTATCATAGAAGACGGCTGAGAGGATCCAAATTAGTCATAA 119
 Db 4070 TCCTGCGATAACTCTTTCGCGTGCCTGCGCTTTCTCATATTGATATTCTGTGAC 4011

Qy 120 TTACTTCTAGTCGGAAACCAACTCGGACCCAAACCCGTCGCTCACCAACTCTGACT 179
 Db 4010 TTTCTCTAACCTTCCACCATATCGGTCTAAAGAGTATTTCTCAGGTTCAGGTGAGC 3951

Qy 180 TAATATACAGACTATGACACTATGACACTATGACATATAAGCTCTGATAGT 239
 Db 3950 CAATTACGGAGTCGGACCTCTGTCATATAAGCTCTCAAGGTGCGCATCTGATA 3891

Qy 240 CCAGATGGAAAATGTTAGGGAACTCAACTAACGGTAAATACTCTCAACTA 299
 Db 3890 CTTCTTGATAACATTATTGTTAGTGAACACTCGTAAAGGTAACATCTGTCACATT 3831

Qy 300 CCTTAGTATAAAATCACATAGTCACAATCGPATCCCTAGTATGATCATCCCTCNA 359
 Db 3830 AGTGAGAAATCCAGAACATGCCGTAAGCATCTCAAGPATCTCAAGTTGCTACTCTCA 3771

RESULT 9
 US-10-427-963-78436/c
 Sequence 78436, Application US/10437963
 Publication No. US2004123343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazutti, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO: 78436
 LENGTH: 2373
 TYPE: DNA
 ORGANISM: Oryza sativa
 FEATURE:
 NAME/KEY: unsure
 LOCATION: (1)..(2373)
 OTHER INFORMATION: unsure at all n locations
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_78243C.1
 US-10-427-963-78436

Query Match 9.0%; Score 129.2; DB 19; Length 2373;
 Best Local Similarity 60.1%; Pred. No. 7e-09;
 Matches 215; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 38 CTTGATATCTGATTTGAGATTTCGATTAAGACTCTPATCTCATAGAGACGCCGCTGCAG 97
 Db 2166 CTCGATTCCTGTTTTCGACAGCGCTGAGCTTCTGCGCTTCTGCGCT 2107

Qy 98 AGGATCCAAATTAGTCATAAAATTATCTCAGTCGGAAACCAACTCGGACCCAAAC 157
 Db 2106 GTGTGTCGTTATCTGCTATCCCTCTGGTGTGTTACCATCGGTCTCAATT 2047

Qy 158 CGCGCGTCACCCAACTCACTGATATAAACAGAGTATGACCTATAGAGC 217
 Db 2046 AGCTTCCTCCCTATGGAAATCCACACATGGATCTGACTCTTCATAAAGTGC 1987
 Qy 218 CTCGTAAGGTGCCATCTAGATGCCAGATGGAAACACTGTATTGTAGGGAACTCAACTAA 277

RESULT 10
 US-10-437-963-78434/c
 Sequence 78434, Application US/10437963
 Publication No. US20040123343A1
 GENERAL INFORMATION:
 i APPLICANT: La Rosa, Thomas J.
 i APPLICANT: Kovalic, David K.
 i APPLICANT: Zhou, Yihua
 i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 i NUMBER OF SEQ ID NOS: 369326
 i SEQ ID NO: 177419
 i LENGTH: 1155
 i TYPE: DNA
 i ORGANISM: Zea mays
 i FEATURE:
 i OTHER INFORMATION: Clone ID: MRT4577_93395C.1
 US-10-425-115-177419

Query Match 9.0%; Score 128.8; DB 20; Length 1155;
 Best Local Similarity 61.2%; Pred. No. 6.7e-09;
 Matches 208; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 58 GATTTGCAATAAGACTTCTATCATAGAAGAGCCCTGCAGAGGATCACAATTAGTCTAA 117
 Db 697 GGTCGCAATACTCTTGGCGATGCTGACCTTCTCATATTGAAATTCTGTCAA 638
 Qy 118 AATATCTTAGTCAGCTTGAAACAACTCAGAACCCGGTGGCTAACCCAACTCAG 177
 Db 637 CCTTTCTTGACCTCTTACCATATCAGGCCAAAGAGTACCTTCTCCAGGTTTCAG 578
 Qy 178 TCTTAATATAACAGAGTATGACACTTATGACCATATGAGCTCGTAAGGGTCCATCTGA 237
 Db 577 ACCATTAGGGAGTTGACACGGTGGCCATAGAAAGTCCAAAAGGTGCACTTGA 518
 Qy 238 TGCAGATGGAACCTGATTGAGGGAACTCAACTAACGTTAAAAAAATCCTCTCAAC 297
 Db 517 TACTTCCTCTATACTGTATTGTATTGTATTGAAAAACTCGCTTAAGGGCAACATCCATT 458
 Qy 298 TACCTTAGTATAAAATCACATGGCTCAAATGPRATCCTCTAGTATATGATCACCTCT 357
 Db 457 TCTTGAGAAGTCAGGATGGAATGCACTTCCAGATTGATTGACCTCT 398
 Qy 358 CAAATGACCATGCTGGCTGAGGATGGAATGCAACGGGT 397
 Db 397 CAGTCGCCACTGTTGGGATGATAAGCCGACTGTG 358

RESULT 12
 US-10-425-115-109131/c
 Sequence 109131, Application US/10425115
 ; Publication No. US20040214272A1
 GENERAL INFORMATION:
 i APPLICANT: La Rosa, Thomas J.
 i APPLICANT: Kovalic, David K.
 i APPLICANT: Zhou, Yihua
 i APPLICANT: Cao, Yongwei
 i TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 FILE REFERENCE: 38-21(5322)B
 CURRENT APPLICATION NUMBER: US/10/425,115
 CURRENT FILING DATE: 2003-04-28
 i NUMBER OF SEQ ID NOS: 369326
 i SEQ ID NO: 109131
 i LENGTH: 4884
 i TYPE: DNA
 i ORGANISM: Zea mays
 i FEATURE:
 i OTHER INFORMATION: Clone ID: MRT4577_31023C.1
 US-10-425-115-109131

Query Match 9.0%; Score 128.8; DB 20; Length 4884;
 Best Local Similarity 61.2%; Pred. No. 9.5e-09;
 Matches 208; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

Qy 338 TAGTATGAAATCACCTCTCAATTCGAGTAAACTTGTGAGGATGAAATGAGACGG 395
 Db 3732 TAAAGTTGAAATGCTGGCTGAGTCCGGTCAAGTCAAGGATCATGATCCTAA 3675

RESULT 11
 US-10-425-115-177419/c
 Sequence 177419, Application US/10425115
 ; Publication No. US20040214272A1
 ; GENERAL INFORMATION:

Qy 58 GATTGATAGACTCTATCTATCAGAGACGCCCTGAGAGTCCAAATTAGTCATAA 117
 Db 4426 GGTCGGATAACTCTTTGCGAGTCGCTTCATATPATGAATTTTATGAA 4367

Qy 118 AATTATCTTCACTGTCGGAAACCACTCGGACCCAACTCGCTAACCTCAG 177
 Db 4366 CCTTTCTGACCTCTTCACTATCAGCTTAAGAGATCTTCTCAGGTTAG 4307

Qy 178 TCTAATATAACAGAGTATGACACTTATGACCATATAGGCCTGTAAGGTGAGA 237
 Db 4306 ACCATTACGGACTTCGACACCGTGCCATATAACCTCAAAGGTGCACTCTGA 4247

Qy 238 TGCCAGATGTCGAACACTGTTATTGTAAGTAACTAACCTAACGTAAATCTCTCAC 297
 Db 4246 TACTTCTGATACTGTTATTGTAAGTAAACTCGTGGAAAGATTGATCCCTT 4187

Qy 298 TACCTTAGTAAATCACTACATAGCTCAAATCGTATCCTCTAGTATGAACTCCTCT 357
 Db 4186 TCTGTGAGATGTCAGAAACATGCCGAGCATTCCTCGAGTGTATTACCTCT 4127

Qy 358 CAAATTGACCATCGGTCTGGGATGGAATGCGAACCGGTRG 397
 Db 4126 CAGCTGTCCACITGTTGGGATGATGCCGAACTGTG 4087

RESULT 13
 US-10-425-115-177411
 Sequence 177411, Application US/10425115
 ; PUBLICATION NO. US2004021427A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; LENGTH: 5433
 ; TYPE: DNA
 ; ORGANISM: zea mays
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(5433)
 ; OTHER INFORMATION: unsure at all n locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_9338C.1
 ; US-10-425-115-177411

Query Match 9.0%; Score 128.4; DB 20; Length 5433;
 Best Local Similarity 61.2%; Pred. No. 1.1e-08;
 Matches 207; Conservative 0; Mismatches 131; Indels 0; Gaps 0;

Qy 60 TTTCGATAGACTCTATCTATCAGAGAGGCCCTGAGGATCCAAATTAGTCATAA 119
 Db 461 TCTGATAACTCTTTGCTGTGAGCTTCTCATATTATGATATTCTGAACT 520

Qy 120 TTATCTTCACTGTCGAACCAACTCGGACCCAAACCGTGGCTCCCCAACTCAGTC 179
 Db 521 TTTCCTTCAACCTCTTCACTATCAGCTTAAGAGTATCTTCAGGTTCAGRC 580

Qy 180 TAATATAACAGAGTATGACCTATGACCATATAGGCCTGTAAGGTGCACTCTAGTG 239
 Db 581 CAATTAGCGGACTTCGACACCGTCTGCTCATATAAGGCTCAAGGGGCCATTTGATA 640

Qy 240 CCAGATTGAAACTCTTATGTCAGGGAACCTCAACTAACGTTAAAAATCCTCTCAACTA 299
 Db 641 CTTCTGGTAGCTPATTATATGAAACTCCGCTAANGTAGACATCCATT 700

Qy 300 CCTTAGATAATAATCAGCTCCAATCGTATCCTAGTATGATATGATCACCTTCTCA 359
 Db 701 AGTGAGAATCCGGACACATGCCGAGATATCTCAAGTATTGTCACCTCTCA 760

Qy 360 AATTGACCATCGSTCTGAGGTCGAACTGAGACGGGNG 397
 Db 761 GTCGCCACTGTTGGGATGATAGCCGAACTGTG 798

RESULT 14
 US-10-298-122-2/c
 Sequence 2, Application US/10298122
 ; PUBLICATION NO. US2003022121A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gmitter, Frederick G.
 ; APPLICANT: Deng, Zhanao
 ; APPLICANT: Zhang, Hongbin
 ; TITLE OF INVENTION: CITRUS TRISTEZA VIRUS AND METHODS OF USE
 ; FILE REFERENCE: 5853-220
 ; CURRENT APPLICATION NUMBER: US/10/298,122
 ; CURRENT FILING DATE: 2002-11-15
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 58965
 ; TYPE: DNA
 ; ORGANISM: artificial
 ; FEATURE:
 ; OTHER INFORMATION: Poncirus trifoliata and Citrus grandis hybrid

Qy 60 TTTGGATAGCTTCTATCTATGAAAGAGCGCTGCACAGGTCCTAACATTACTCTAAA 119
 Db 44765 TCTCATAGCTCTGTCTATCTGGCCACTTTAATCTACCCGAAATCATGTATGATC 44706

Qy 120 TTATCTTCACTGTCGCTGCTCACCCAACTCAGGACCCAAACCCGTCGCTCACCCAACTCAGTC 179
 Db 44705 TTCTCATCTCATCTGCTGATTTCTGACCCATAACCTCTGTCACCAAACCTCATCC 44646

Qy 180 TAATATAACAGAGTATGACCTATGACCATATAGGCCTGTAAGGTGCACTCTAGTG 239
 Db 44645 CAACATCTGGTCTCTGGATGATAGCCATATAAGGCTCATACAAGGCTCATACAAGGCT 44586

Qy 240 CCAGATTGAAACTCTTATGTCAGGGAACCTCAACTAACGTTAAAAATCCTCTCAACTA 299
 Db 44585 CTAGCTGATAACTGTTGTTGTAAGCAAACTCCATCAGGTAATAATTGTCACATT 44526

Qy 300 CCTTAGATAATAATCAGCTCCAATCGTATCCTAGTATGATATGATCACCTTCTCA 359
 Db 44525 CCTTTAAACTCCATACACAAGGCTCATAGCTGATGATAGCTGTC 44466

Qy 360 AATTGACCATCGTCTGAGGATGGATG 387
 Db 44465 GACTGTCCTCATGCTCTGGATGAAG 44438

RESULT 15
 US-10-425-78438/c
 Sequence 78438, Application US/10437963
 ; PUBLICATION NO. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovacic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei

```

i APPLICANT: Wu, Wei
i APPLICANT: Boukharov, Andrey A.
i APPLICANT: Barbuzuk, Brad
i APPLICANT: Li, Ping
i TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
i Plants and Uses Thereof for Plant Improvement
i FILE REFERENCE: 38-21 (53221)B
i CURRENT APPLICATION NUMBER: US/10/437,963
i NUMBER OF SEQ ID NOS: 204566
i SEQ ID NO: 78438
i LENGTH: 4641
i TYPE: DNA
i ORGANISM: Oryza sativa
i FEATURE:
i OTHER INFORMATION: Clone ID: PAT_MRT4530_78245C.1
US-10-437-963-78438

Query Match          8.8%; Score 126; DB 19; Length 4641;
Best Local Similarity 59.5%; Pred. No. 2.3e-08;
Matches 213; Conservative 0; Mismatches 145; Indels 0; Gaps 0;
Qy      38 CTTGATATCTATGATTTCAGATTGCTATAAGACTCTATCTATGAAAGACGGCTGCAG 97
Db      4161 CTCATATTCTCGTCCTCTGACATCGCTGTACTTCGCTACTTGTGACTGCTGCAAGCAT 4102
Qy      98 AGGATCCAAATTAGCTAAATTATCTCAGTCTTGAAACCACTAGAACCCRAAAC 157
Db      4101 GTGTTGTCGATTCTCTGATTCGGTTCTGTTGCTGTTGACCCACGGGTCTTAAGAT 4042
Qy      158 CGGTGCTCTACCCCAACTCAGCTCTAATAACAGACTATGACATATAGCCATAGGCC 217
Db      4041 AGCTCTCTCCCTATGGAACTCCAAACAATGGGATGACATTCCTCCATAAGTGC 3982
Qy      218 CTCGTAAGGTCCATCTAGATGCCAGATTGAAACTGTTATTGAGGGAACTCAACTAA 277
Db      3981 CTCATATGGTCCATTGTAATGCTGAACTATGCTGAAACTATGTTGAAAGAAATTCTPACAAG 3922
Qy      278 CGGTAAAAAAATCCTCTCAACTACCTTGTATAAAATCACATAGCTCAAATCGPATCTC 337
Db      3921 CGGCATATGATCTCCAACTGCTTCAGATGCTTCCATGAAGGATCATGATCTCACATCTC 3862
Qy      338 TAGTATGAAATCACCTCTCAAAATGACCATGGATGCAATGAGCCATGAGCGG 395
Db      3861 TAAAGTTGAAATGCTGAGTGGCTGAGTGGCTGAAAGCGTACTG 3804

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Search completed: August 13, 2005, 22:17:26
Job time : 8245 secs

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OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 18:33:08 ; Search time 1232 Seconds
 (without alignments)
 6885..543 Million cell updates/sec

Title: US-10-089-543-2

Perfect score: 1433

Sequence: 1 actataggccacgcgtggc.....tgagagaatccctcacatc 1433

Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Searched: 439026 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqm2000s:*
- 4: geneseqn2001as:*
- 5: geneseqm2001bs:*
- 6: geneseqm2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqm2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqm2004bs:*
- 13: geneseqn2004bs:*

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1433	100 0	1433	6	ABK15699	Cotton fi	Abk15699 Cotton fi
2	120	8.4	200	8	ADA71742	Rice gene	Ada71742 Rice gene
3	113.8	7.9	31491	4	AAD10203	Pepper	Aad10203 Pepper
4	113.8	7.9	31491	4	AAF613301	Pepper	Aaf613301 Pepper
5	113.8	7.9	31491	6	AAK98833	Nucleic a	Aak98833 Nucleic a
6	107.4	7.5	8056	8	ABZ10246	Haematopo	Abz10246 Haematopo
7	105.8	7.4	8056	8	ABZ10100	Haematopo	Abz10100 Haematopo
8	105	7.3	8222	8	ACF62816	Colon can	Acf62816 Colon can
9	105	7.3	11222	10	ADB54318	Preverte	Adb54318 Preverte
c 10	105	7.3	59590	3	AAF22281	BAC conta	Aaf22281 BAC conta
c 11	104.8	7.3	158001	12	ADL1784	Human pho	Adl1784 Human pho
c 12	104.4	7.3	4985	6	ABQ75107	Anophilos	Abq75107 Anophilos
c 13	104.4	7.3	4985	10	ACF79720	Mosquito	Acf79720 Mosquito
c 14	103.8	7.2	163319	3	AAFF22306	Arabidops	Aaff22306 Arabidops
c 15	103.4	7.2	8222	8	ACF62794	Colon can	Acf62794 Colon can
c 16	103.4	7.2	11222	10	ADB54190	Preverte	Adb54190 Preverte
c 17	102.4	7.1	2000	12	ADJ41131	Plant cDN	Adj41131 Plant cDN
c 18	101.2	7.1	109973	3	AAF22288	BAC conta	Aaf22288 BAC conta
c 19	101.6	7.1	8056	8	ABZ10246	Haematopo	Abz10246 Haematopo
c 20	101	7.0	110000	3	AAFP22305_08	Continuation (9 of	The invention relates to a promoter that is cotton fibre-specific,

ALIGNMENTS

RESULT 1	
ID	ABK15699 standard; DNA; 1433 BP.
XX	
AC	ABK15699;
XX	
DT	21-MAY-2002 (first entry)
XX	
DB	Cotton fibre-specific beta tubulin, CFTUB2, promoter fragment.
XX	
KW	Cotton; ds; CFTUB2; fibre-specific beta tubulin; transgenic. promoter;
KW	plant; anthocyanin gene; silk protein gene; cotton fibre strength;
KW	polyhydroxybutyrate.
XX	
OS	Gossypium hirsutum.
XX	
FH	Location/Qualifiers
FT	449..1433
FT	/*tag=^a
FT	/note= "Cotton fibre-specific promoter. This sequence is specifically claimed in claim 3"
XX	
XX	WO200210377-A1.
XX	
XX	07-FEB-2002.
XX	
PF	01-AUG-2000; 2000WO-SG000111.
XX	
PR	01-AUG-2000; 2000WO-SG000111.
XX	
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.
XX	
PI	Cai L, Li X, Cheng N, Liu J;
XX	
DR	WPI; 2002-217120/27.
XX	
PT	New fiber-specific beta-tubulin promoter from cotton for controlling gene expression in cotton fibers and creating transgenic plants, in particular cotton plants, having altered fiber characteristics.
PT	
PT	Claim 2; Fig 2; 30pp; English.
PS	
XX	

age 2

comprising the promoter of the cotton beta-tubulin gene CFTUB2. The promoter is fibre-specific in cotton and controls specific gene expression at the transcriptional level in cotton fibres and is useful for improving cotton fibres to create new cotton varieties with high fibre quality and yield by gene manipulation. The promoter is useful for creating transgenic plants, in particular cotton having altered fibre characteristics, and permits selective expression of a transgene in the cotton fibre, permitting greater latitude in the types of transgenes employed. Examples of expression of desirable genes in cotton fibre, but not in other parts of the cotton plant, include anthocyanin genes for coloured cotton, silk protein genes from silk worm or spiders for increased strength of cotton fibre, and biosynthesis of polyhydroxybutyrate in cotton fibre for improved thermal properties and insulating characteristics. The promoter can improve cotton fibres to create new cotton varieties with higher fibre quality and yield. The present sequence is the CFTUB2 promoter fragment

Query Match Score 1433; DB 6; Length 1433;
 Best Local Similarity Pred. No. 8.1e-189;

Query Match Score 1433; DB 6; Length 1433
 Best Local Similarity Pred. No. 8.1e-189;

Best local Similarity 100.0%; Freud NO. 0.1e-103; Mismatches 0; Indels 0; Gaps Matches 1433; Conservative 0;

1 ACTATAGGGCA CGCGTGTGCA CGGCCGGCTGGCTTGATATCTATGATTTCAGAT

61 TTGCATAAGACCTCTATCTATCGAAAGACGGGATCCAAATTAGCTAAAAAT
61 TTGCATAAGACCTCTATCTATCGAAAGACGGGATCCAAATTAGCTAAAAAT

61 TTGCATAAGACTCTATCTATCGAAGACGCCGAGGATCCAAATTAGCTAAAAAT
121 TATCTTCAGTCTCGAAACCAAATCAGGACCCAAAACCCGTCAGGGATCCCCAACTCAGCTT

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121 TACCTCTGGAAACCAAATCAGGACCCAAAACCGTCCGTCCCCAACCTAGCT
121 TACCTCTGGAAACCAAATCAGGACCCAAAACCGTCCGTCCCCAACCTAGCT

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181 AATATAACAGACTPATGACACTATGACCATAATAGCCCTCGTAAAGTGCCATTAGATGC

241 CAGATTGAAACTGTATTGTAGCGAACTCAACTAACGTTAAAAATCCCTCAACTAC

241 CAGATTGAAACTGTATTGTAGGGAACTCAACTAACGGTAAAAATCCTCTAACTAC

3001 CTTAGTAATAATCACATAGCTCCAATCGTATCCTAGTATGAAATCCACCTCTCAA
Y

301 CTTAGTAATAATCACATAGCTCAAATCGTATCCTCTAGTATATGAAATCCCTCTCA

361 ATTGACCATGGCTCTGAGATGGAAATCGAGCCGTGCCACGGATTACTATGGTACCT
421 ATTTAATTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT

421 ATAAAAAAATTATTATTATTTTTAAATGATGCAACCAAGTGGTGGAGAGAGAGCTAC
421 ATAAAAAAATTATTATTATTTTTAAATGATGCAACCAAGTGGTGGAGAGAGAGCTAC

421 ATAAAAAATTATTATTATTTTTAAAGAAATTGTAGTGACCAAGTGCTGAGATTGAGAGGTTAC
481 CGATGGTCAAAGGGACCAAATTTTTATTTTACCTCTGCCPAGATTGTAATACTAT

	Y	Y
481	CGAAGGGCAAGGCGACAAAGGAACTTCTGCTGTTATTTTGATTTCCTGCCTAGATTCTGTAAATCTAT	CGAAGGGCAAGGCGACAAAGGAACTTCTGCTGTTATTTTGATTTCCTGCCTAGATTCTGTAAATCTAT
481	CGATTGGTCAGTGGCCAATTTTTATTTCCTGCCTAGATTCTGTAAATCTAT	CGATTGGTCAGTGGCCAATTTTTATTTCCTGCCTAGATTCTGTAAATCTAT

541 TGCATTTATCTCATTTATTAAATTATTTATTGGATAAAATTCTA
542 CCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG

541 TGCATTATCTCATTCATTATTAAATTATTGGATAAATTCTA

601 ATACTTTACTTTTTAAAAGGATTATTATTATTATTAAAT

601 ATACTTACTTTTTAAAAAGATTAAATTATTTAGATAAAAAT

661 TCTAATACTTTACTTTAAAAGAAATTCAATTGCGTTTCTTAATTAGTTT

Db	721	TAATCTPATACTAAATTATAAATTCGTGCGGATAGTGTGGTCAAAGTCAGTCAC	780
Qy	781	ATGAAATTCTGAGAAAAAAATAAAAACATTCTGATTAACTTATTTATATA	840
Db	781	ATGAAATTCTGAGAAAAAAATAAAAACATTCTGATTAACTTATTTATATA	840
Qy	841	TATATAATATAAAACAGTTTTATTAAIGTTGCAATAATATTTTTAATTAAATT	900
Db	841	TATATAATATAAAACAGTTTTATTAAIGTTGCAATAATATTTTAAATTAAATT	900
Qy	901	CACCAACACAATTACACTCTCATCATAAAATTAACTCTTATTACATAATTAA	960
Db	901	CACCAACACAATTACACTCTCATCATAAAATTAACTCTTATTACATAATTAA	960
Qy	961	AGGAAATTATTTTTAATTCACCCCTCAATTAACTTAAATGCATATTAACTT	1020
Db	961	AGGAAATTATTTTTAATTCACCCCTCAATTAACTTAAATGCATATTAACTT	1020
Qy	1021	CTCTCTTATTCACTCCPAACATTAACTTAACTCCAAATTGAACTGTATA	1080
Db	1021	CTCTCTTATTCACTCCPAACATTAACTTAACTCCAAATTGAACTGTATA	1080
Qy	1081	ACTTAACTCAATTCAATTGTTGCTCATCTGGTCCATTCTGGTCAAGGTCAAC	1140
Db	1081	ACTTAACTCAATTCAATTGTTGCTCATCTGGTCCATTCTGGTCAAGGTCAAC	1140
Qy	1141	CACACTTGGCACAGCTCATCAATTCCAGTAACCTAACATGTTACAGTT	1200
Db	1141	CACACTTGGCACAGCTCATCAATTCCAGTAACCTAACATGTTACAGTT	1200
Qy	1201	AATTCAAAAATTCCAGAAACGAAAGCTCGTTACTAACCGACCTAAACC	1260
Db	1201	AATTCAAAAATTCCAGAAACGAAAGCTCGTTACTAACCGACCTAAACC	1260
Qy	1261	CAGCTCAACCTGGCTGCAATTACGGAAATCTTAACTCTCTATAAACCA	1320
Db	1261	CAGCTCAACCTGGCTGCAATTACGGAAATCTTAACTCTCTATAAACCA	1320
Qy	1321	CTCTCATCACCATTCCCCATAAAAGAAATTCCGGAAATTCTTATATT	1380
Db	1321	CTCTCATCACCATTCCCCATAAAAGAAATTCCGGAAATTCTTATATT	1380
Qy	1381	CCTCTCCAATTTCGGTCACTTCCGGAAAATGAGAAATCCTTCACATC	1433
Db	1381	CCTCTCCAATTTCGGTCACTTCCGGAAAATGAGAAATCCTTCACATC	1433
RESULT 2			
	ADA71742	Standard; DNA; 2000 BP.	
	ID	ADA71742	
	XX		
	AC	ADA71742;	
	XX		
	DT	20-NOV-2003 (first entry)	
	XX		
	DB	Rice gene, SEQ ID 5067.	
	XX		
	KW	Plant; bacterial infection; fungal infection; viral infection; rice;	
	KW	gene; ds.	
	XX		
	OS	Oryza sativa.	
	XX		
	PN	WO2003000898-A1.	
	XX		
	PD	03-JAN-2003.	
	XX		
	PF	22-JUN-2001; 2001WO-1B001105.	
	XX		
	PR	22-JUN-2001; 2001WO-1B001105.	
	XX		
	(SYGN)	SYNGENTA PARTICIPATIONS AG.	
	PI	Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;	

PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
 XX DR; 2003-175290/17.

XX Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant to bacterial, fungal or viral infection by determining or detecting plant gene expression.

XX PS Claim 27; SEQ ID NO 5067; 899pp; English.

XX The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

XX Sequence 2000 BP; 569 A; 433 C; 409 G; 589 T; 0 U; 0 Other;

SQ Query Match 8.4%; Score 120; DB 8; Length 2000;
 Best Local Similarity 60.4%; Pred. No. 4.9e-08;
 Matches 198; Conservative 0; Nismatches 130; Indels 0; Gaps 0;

QY 63 GCATAGAGCTCATATCATATCGAAAGCGCTCGACAGGATCCAAATTAGTCATAATA 122
 Db 421 GCGTAATTCCTCTGAGGTCTGAGTCTGCTGTTCTCAAGCTCTGTATCAGCTAACCTGT 480

=QY 123 TCTTCAGTCGGAAACCAACTCAGGACCCRAAACCGGTGCTCAGCCAACTCAGTCATA 182
 Db 481 TCTTCAGTCGACTTGAGTATGAGCAACCTATGACCATATAGAGCTCATAGTCATA 540

QY 183 TATAACAGAGTATGACCATATGACCATATAGAGCTCATAGTCATACTGCCTGCCACCTCG 540
 Db 541 CATAAGGAGTAGGGCACTTCCTCGAACATTCAGCCATTGCTCGGGACATCTGATCTG 600

QY 243 GATTGGAACCTGTATTGAGGGAACCTCAACTAAGTAAAAAATCTCTCAACTACTCT 302
 Db 601 GCCTGATAGCTGTGTGTATGAGAACCTGAGCATCGCAACACGATCCCTAGTGCT 660

QY 303 TAGTAAATAATCACATAGCTCCAATCTGATPATATGATACCTCTCAAT 362
 Db 661 TCGAARATCCAGGGCACGCGATGCTTACCGTTACCCCTCTGTC 720

QY 363 TGACCCATGGCTCTGAGGATGAAATGCC 390
 Db 721 TGACCCATGGCTCTGCGATGTAGGGCG 748

RESULT 3
 AAD10203 ID AAD10203 standard; DNA; 31491 BP.
 DT 24-SEP-2001 (first entry)
 DB Pepper Bs2 gene.
 XX Bs2 gene; Pepper; resistance gene; plant pathogen; virulence gene;
 KW bacterial spot disease; Xanthomonas campestris pv. vesicatoria; AvrBs2;
 KW hypersensitive response; transgenic plant; tomato; tobacco; rice; corn;
 KW wheat; ds.
 OS Capsicum annuum.
 XX Key Location/Qualifiers
 FT promoter 1. .502 / *tag= a
 FT

FT exon 503. .554 / *tag= b
 FT /number= 1 /note= "This region contains a portion of 5' untranslated region (5' UTR)"
 FT intron 555. .1439 / *tag= c /number= 1 /note= "The 5' untranslated region (5' UTR) continues in this region"
 FT exon 1440. .4162 / *tag= d /number= 2 /note= "The region 1440-1479 contains 5' UTR which is followed by the coding region"
 FT CDS 1480. .31219 / *tag= e /product= "Bs2 protein"
 FT intron 4163. .31184 / *tag= f /number= 2 /note= "This region" 31185. .31216 / *tag= g /number= 3 /note= "The region 31185-31216 contains 5' UTR which is followed by the coding region"
 FT exon 31220. .31491 / *tag= h /note= "The region 31220-31491 contains 5' UTR which is followed by the coding region"
 PN US5262343-B1.
 PD 17-JUL-2001.
 PP 23-JUL-1999; 99US-00360186.
 PA (RESCC) UNIV CALIFORNIA.
 PI Staszkowicz BJ, Dahlbeck D, Tai TH;
 PR 23-JUL-1998; 98US-0033957P.
 DR 2001-450496/4B.
 DR P-PPDB; AAB05309.
 XX Nucleic acid molecules encoding Bs2 protein, useful for producing transgenic plants having resistance to the plant pathogen Xanthomonas campestris.
 PS Claim 7; Col 21-50; 379pp; English.
 XX The present sequence is Bs2 gene from pepper. The Bs2 gene is shown to confer resistance to plant pathogen Xanthomonas campestris pv. vesicatoria which causes bacterial spot disease. The Bs2 protein has Bs2 biological activity, i.e., when co-expressed in a plant with a X. campestris AvrBs2 gene product, it produces a localised hypersensitive response. The protein includes a nucleotide binding motif and leucine rich repeats of the type found in other plant resistance genes. The Bs2 nucleic acid molecule is useful for producing transgenic plants such as pepper, tomato, broccoli, cauliflower, cabbage, cowpea, grape, canola, bean, soybean, rice, corn, wheat, barley, citrus, cotton, cassava and walnut, that are resistant to plant pathogen Xanthomonas campestris. The transgenic plants produce using Bs2 molecule develop a hypersensitive response to the pathogen at the site of inoculation and show an enhanced resistance to systemic infection. The Bs2 nucleic acid molecule is also useful as polymerase chain reaction (PCR) primers for amplifying portions of Bs2 nucleic acid molecule, as sequencing primers to verify the authenticity of an amplified molecule, and as hybridisation probes
 SQ Sequence 31491 BP; 9652 A; 6344 C; 5992 G; 9503 T; 0 U; 0 Other;
 Query Match 7.9%; Score 113.8; DB 4; Length:31491;
 Best Local Similarity 59.5%; Pred. No. 2.7e-07;
 Matches 210; Conservative 0; Mismatches 142; Indels 1; Gaps 1;

PT exon /number= 2
 PT 3185 .31216
 PT /*tag= h
 PT /number= 3
 PT 31219 .31491
 PT /*tag= i
 PT /note= "3'UTR and 3' regulatory region"
 XX US2002012981-A1.
 XX 31-JAN-2002.
 XX 24-MAY-2001; 2001US-00864680.
 XX 23-JUL-1998; 98US-0093957P.
 XX 23-JUL-1999; 99US-00360186.
 PA (STAS/) STASKAWICZ B J.
 PA (DEHL/) DEHLBICK D.
 PA (TAIT/) TAI T H.
 XX Staskawicz BJ, Dahlbeck D, Tai TH;
 XX DR WPI: 2002-205100/26.
 DR P-PSDB; AAO19973.
 PT New Capsicum annuum protein with Bs2 protein biological activity, useful
 PT for conferring or enhancing resistance of plants (e.g. tomato, cabbage,
 PT broccoli, cotton, grape, rice or walnut) against the pathogen Xanthomonas
 PT campesstris.
 XX Claim 3: Page 12-26; 39pp; English.
 CC The invention relates to nucleic acid molecules (CDNAs and genes) that
 CC confer resistance to the plant pathogen Xanthomonas campesstris. The
 CC invention more specifically relates to an isolated Capsicum annuum
 CC (pepper) protein and its encoding polynucleotide. The protein is useful
 CC for conferring or enhancing resistance of plants (e.g. pepper, tomato,
 CC cabbage, broccoli, cauliflower, cowpea, cotton, cassava, grape, corn,
 CC rice, soybean or walnut) against the plant pathogen Xanthomonas
 CC campesstris. This polynucleotide sequence represents the Capsicum annuum
 CC BS2 gene of the invention.
 XX Sequence 31491 BP; 9652 A; 6344 C; 5992 G; 9503 T; 0 U; 0 Other;
 CC Query Match 7.9%; Score 113.8; DB 6; Length 31491;
 CC Best Local Similarity 59.5%; Pred. No. 2.7e-07;
 CC Matches 210; Conservative 0; Mismatches 142; Indels 1; Gaps 1;
 CC
 Qy 38 CCTGATCATCTGTTCAAGTTCAGATTGCGATAAGCTCTATCTATGAAAGCCTGCAG 97
 Db 22086 CTCTAGTCCTCCTCCGAAACTCGGATAGACATGGACATTAAGACTATGAGCTTGAC 22145
 Qy 98 AGGATCCAAATTAGCTTAAATTATTCAGTCCTGGAACCAACTCAGGACCCAAAC 157
 Db 22146 TCG-TCTTAATGTTCACTTCTCACTGGACCTATCCATCTTGTGAACTGACATCAA 22204
 Qy 218 CTCGTAAGGTGCCATCTAGATGCCAGTTGAAACTGTTATGGAACTCAACTAA 277
 Db 22265 CTCAAAGGGCATCTGAGTCGATGGTAGTATTATGGAACTGAACTTCACTGCAG 22324
 Qy 278 CGGTAAAATTCATCCCTCAACTACCTCTGTTAATAATCACATAGCTCAATCGTCRC 337
 Db 22325 TGGCAAGTGTATCCCAACTACCTCTGAACTGAACTTCAATCACATTC 22384
 Qy 338 TAGTATGAACTACCTCTCAATTGACCATCGGTGTTGAGTGAATGCAATGAG 390
 Db 22385 GRGGCTCTGAATGGTAGCTAGCTTCACTCCGTTGAGGTGAAACCTG 22437

RESULT 6
 ID ABZ10246 standard; DNA; 8056 BP.
 XX
 AC ABZ10246;
 XX DT 16-JAN-2003 (first entry)
 XX DE Haematopoietic cell proliferation disorder related DNA sequence #386.
 XX KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; gene; ds.
 XX OS Homo sapiens.
 XX PN -WO200277272-A2.
 XX PD 03-OCT-2002.
 XX PF 26-MAR-2002; 2002WO-EP003401.
 XX PR 26-MAR-2001; 2001US-0278333P.
 XX (EPIG-) EPIGENOMICS AG.
 XX PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olein A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E,
 PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C,
 PI Schwae I, Ziebarth H;
 XX DR WPI: 2003-016942/01.
 XX Detecting and differentiating between hematopoietic cell proliferative disorders
 PT associated with at least 1 gene and/or their regulatory regions in a
 PT subject. The method comprises contacting a target nucleic acid in a
 PT biological sample obtained from the subject with at least 1 reagent,
 PS which distinguishes between methylated and non-methylated CpG
 XX Claim 28; SEQ ID NO 386; 117pp; English.
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ11118 to ABZ09851
 CC represent specifically claimed sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
 CC Query Match 7.5%; Score 107.4; DB 8; Length 8056;
 CC Best Local Similarity 51.1%; Pred. No. 2.3e-06;
 CC Matches 305; Conservative 0; Mismatches 286; Indels 6; Gaps 2;
 CC Qy 500 AAATTTTTTATTTTACTCCCTGCTTACATTGCTTAATACTATTGCAATTCTCAT 559
 CC 55 AAATTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAAT 114

Qy	560	TATTTTATTATTTATTTATTTATTTATTTATTTGATAAAATTCTAATACCTTACTTTTTAA	619	CC	Claim 28; SEQ ID NO 240; 117pp; English.
Db	115	TATTTTATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTT- -	172	PS	
Db	620	AAGAATTCTAATTAATTCTAATTTATTTATTTATTTATTTATTTATTTATTTATTT- -	679	CC	The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AB209861 to AB211118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferative disorders related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients.
Db	173	TATTTTATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT- -	232	CC	
Db	680	TTAAAGAATTCTAATTAATTCTAATTTATTTATTTATTTATTTATTTATTTATTT- -	739	CC	
Db	233	ATTTTAAAATTCTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT- -	292	CC	
Qy	740	AAATTCTGATGGATTAGTGCGTCAAAGTCAACTCATGAATTGTGGAGAAA	799	CC	
Qy	293	ATTTTTTAAATTCTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT- -	352	CC	
Db	800	AAATAAAAATTAAACACATTTCGATTAACCTTATTTATTTATTTAAACACAT	859	CC	
Db	353	ATTAATAAAATTAATGATAAAATTATAATTATAATTATAATTATAATTATAATTAT- -	412	CC	
Qy	860	TTTATTTAATCT---TGTCTAAATAATTCTAATTTCAATTTCAGCACAAATTAC	915	CC	
Db	413	ATTTATTAATTTATTATTTATTATTTATTTATTTATTTATTTATTTATTTATTT- -	472	CC	
Qy	916	ACTCTCATCTAAATTAACTTCTTAACTTAAATTGTGGAGCAATTATTT	975	CC	
Db	473	ATATATTTAAATAAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAT- -	532	CC	
Qy	976	TAATCTCACCCTCCATTAATGCTATTTGTCGATCTCTTATTTCACTC	1035	XX	
Db	533	TAATAATTAAATTATAATTATAATTATAATTATAATTATAATTATAATTATAATT- -	592	XX	
Qy	1036	CTAACATTAATTAACCAATTTCGAACTTCAACTTCTTAACCTTCACTA	1092	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	593	ATAATATTTAAATAAAATTATAATTATAATTATAATTATAATTATAATTATAATT- -	649	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Db	500	AATTTTTATTATTTACCTCCCTGGCTTAGATTCGTAATAACTATTGCATTTCATTTCAT	559	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	55	AAATTTTTTTTTATTATTTATTATTTATTATTTATTATTTATTATTTATTATTTATTATTT- -	619	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	560	TATTATTAATTATTATTATTTATTGGATAAAATTCTAATCTTACTTTTTAA	619	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	115	TATTATTTAATTATTATTATTTATTATTTATTATTTATTATTTATTATTTATTATTT- -	172	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	620	AAAGGATTATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATT- -	679	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	173	TATTATTTTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	232	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	680	TTAAAAGAATTCTAATTCGTTTTCTTAATTAGTTTAATTCTATACTAAATTATA	739	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	233	ATTTTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	292	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	740	AAAATTCTGATGGATTAGTGCGTCAAAGTCAGTCACATGAAATTCTGGGAAAA	799	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	293	ATTTTTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	352	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	800	AAATAAAAATTAAACCAATTTCGATTAATCTTAACTTAAACACAT	859	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	353	ATTAATAAAATTAACCAATTTCGATTAATCTTAACTTAAACACAT	812	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	860	TTTATTAAATGT-- -TGTCAATTAAATTATTTAAATTAAATTAAATTAAATTAA	915	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	413	ATTTATTAAATTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	472	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	916	ACTCTCATCTAAATTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT	975	Qy	Query Match 7.4%; Score 105.8; DB 8; Length 8056;
Db	473	AAATATTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	532	Db	Best Local Similarity 50.9%; Pred No. 3.9e-06; Mismatches 0; Indels 6; Gaps 2; Matches 304; Conservative
Qy	976	TAATCTCACCCTCCATTAATGCTATTTGTCGATCTTCACTTCATTCTCACTC	1035	XX	
Db	533	TAATAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	592	XX	
Qy	1036	CTAACATTAAATCTAACCAATTTCGATTTGTCGATCTCTTATTTCACTC	1092	Qy	(EPIG-) EPIGENOMICS AG.
Db	593	ATAATTTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAAATTAA	649	Db	Detecting and differentiating between hematopoietic cell proliferative disorders, comprising contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

RESULT	8	ACF62816	ACF62816	Colon cancer analysis related genomic DNA SEQ ID NO:65.
ID	ACF62816	standard;	DNA;	8222 BP.
XX	XX			
DE	XX			
KW	Human; colon; cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;			
KW	progesterone receptor; p53a; CEA; c-erb2; c-erbB2; methylation; CpG;			
KW	characterisation; classification; diagnosis; differentiation;			
KW	colon cell proliferative disorder; gene; ds _B .			
XX	XX			
OS	Homo sapiens.			
OS	Synthetic.			
XX	XX			
PN	PN			
XX	XX			
PD	PD	20-FEB-2003.		
XX	XX			
PF	PF	09-AUG-2002; 2002WO-EP008939.		
XX	XX			
PR	PR	09-AUG-2001; 2001DE-01039283.		
XX	XX			
(EPIG-) EPIGENOMICS AG.				
PA				
XX				
P1	P1	Distler J, Model F, Taubert H;		
XX	XX			
DR	DR	WPI: 2003-256600/25.		
XX	XX			
PT	PT	Determining methylation status of CpG dinucleotides using modified genomic sequences, oligonucleotides and/or RNA-oligomers, useful in the characterization, grading, staging and/or diagnosis of colon cancer.		
PT	PT			
PT	PT			
XX	XX			
PS	PS	Claim 22: Page 115-117; 219pp; English.		
XX	XX			
CC	CC	The present invention describes a method for determining the methylation status of CpG dinucleotides within the genes for oestrogen receptor, p21		
CC	CC	p27, p16, progesterone receptor, myoglobin, p53a, c-erb2, p53		
CC	CC	and/or CEA, which comprises contacting the target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides, and determining from the methylation status of the CpG positions the presence of a colon cancer. A set of oligomers or peptide nucleic acid (PNA)-oligomers can be used as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNP) of a corresponding genomic DNA by analysis of a chemically pretreated genomic DNA. The pretreated genomic DNA is useful for the determination of the methylation status of a corresponding genomic DNA and/or detection of SNPs. The methods and pretreatment of genomic DNA are also useful for the characterisation, classification, diagnosis and differentiation of colon cell proliferative disorders. ACF62752 to ACF63278 represent sequences used in the exemplification of the present invention.		
CC	CC			
XX	XX			
SQ	Sequence 8222 BP; 2010 A; 0 C; 1769 G; 4443 T; 0 U; 0 Other;			
Query	412	ATGGTACCTATAAAAATTATTATTTTAAATTGATGAGCACCAGTGTTGGGAGAGA	47	
Best Local Similarity	7.3%	Score 105; DB 8; Length 8222;		
Matches	345;	Mismatches 0; Pred. No. 5e-06;		
Conservative	49.9%;	Indels 6; Gaps		
Db	7223	ATGGTGTGTTGTTGTTGATTGATTAATGGTTATTGATTAATGGTGTGTT	72	
Query	472	GAGCTCTACCGATGGTCAGTGCACTGATTATTACTCTGCCTGATTCTGATTCG	53	
Db	7283	TTGTAAGAAAGAGTGAGGATGATTGTTATTATTTATGTTATTGTTTTT	73	
Query	532	AAACTATGCTATTCTCATTCATTATTATTATTATTATTATTATTATTATT	58	
Db	7343	AATTATTTAGTTATTATTATTATTATTATTATTATTATTATTATTATT	74	

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1433	100.0	1433	6	AX370650		AX370650 Sequence
2	1393.8	97.3	5765	8	AF487511		AF487511 Gossypium
C	3	266	18.6	572	8	AF025353	Gossypium
C	4	184	12.8.	300	8	AF060583	Gossypium
C	5	179.4	12.5.	598	8	AY181254	Gossypium
C	6	179	12.5	913	8	AF276939	Gossypium
C	7	156.4	10.9	927	8	AF277099	Gossypium
C	8	150.6	10.5	111063	2	AC146584	Medicago
C	9	140.2	9.8	121257	2	AC146307	Medicago
C	10	139.8	9.8	119220	2	AY508219	Medicago
C	11	139	9.7	96930	8	AC149484	Populus b
C	12	137.6	9.6	78069	2	AC150760	Medicago
C	13	137.4	9.6	141416	8	AC149480	Populus b
C	14	137.2	9.6	143392	8	AC149299	Populus b
C	15	136.4	9.5	107287	2	AC146794	Medicago
C	16	136.4	9.5	181249	2	AC148479	Zea may
C	17	135.6	9.5	65157	2	AC148403	Medicago
C	18	135.6	9.5	123241	2	AY379775	Medicago
C	19	135.4	9.4	106114	2	AC146565	Medicago

Db	61	GAGGATCCAAATTAGCTAAATTATCTTGAGTCGGAAACACTCAGGACCCAAA	120	Qy	1237	TCCGTTACTAACCGACCTAAACCCAGCTAACCTGCCGTOAAATTAAACGGAAATTCTTTTA	1296
Qy	157	CCCGTCCTACCCAAACTCAGTCCTAAATTACAGAGTATGACCTTATGAG 216		Db	1201	TCCGTTACTAACCGACCTAAACCCAGCTAACCTGCCGTOAAATTAAACGGAAATTCTTTTA	1260
Db	121	CCGTCTCACCAACTCAGTCCTAAATTACAGAGTATGACCTTATGAG 180		Qy	1297	ACTCCCTCTATAACCAACCACTCTCATCCATTCCCATTAAGAATTTCGGG	1356
Qy	217	CCTCGTAGGTCCTAGATGCCAGATTGAACTGTATTGTAGGGAAACTACA	276	Db	1261	ACTCCCTCTATAACCAACCACTCTCATCCATTCCCATTAAGAATTTCGGG	1320
Db	181	CCTCGTAGGTCCTAGATGCCAGATTGAACTGTATTGTAGGGAAACTACA	240	Qy	1357	AATTCTTAACTCTTCTTCTTCTCCCTCAATTCCCTCAATTCTCCGAGAAATGA	1416
Qy	277	ACGGTAAAATTCTCTCAACTACCTTAAGTATAATTACAGTCTCAAATCGTATCT	336	Db	1321	AATTCTTAACTCTTCTTCTTCTCCCTCAATTCTCCGAGAAATGA	1380
Db	241	ACGGTAAAATTCTCTCAACTACCTTAAGTATAATTACAGTCTCAAATCGTATCT	300	Qy	1417	GAGAAATCCCTCACATC	1433
Qy	337	CTAGTATATGATCACTTCCTCAAATTGACCATCGGATGGAACTGAGCGGT	396	Db	1381	GAGAAATCCCTCACATC	1397
Db	301	CTAGTATATGATCACTTCCTCAAATTGACCATCGGATGGAACTGAGCGGT	360				
Qy	397	GCCACGGATTACTAACTGTTACCTATAAAATTATTTAAAAAATTGATGTGAC	456				
Db	361	GCCACGGATTACTAACTGTTACCTATAAAATTATTTAAAAAATTGATGTGAC	420				
Qy	457	CAGTGGTGGAGAGGGTACCCATTGTCAGTGGACCAATTTTTATTTTACCT	516				
Db	421	CAGTGGTGGAGAGGGTACCCATTGTCAGTGGACCAATTTTTATTTTACCT	480				
Qy	517	CCTGCCCTAGATTCGTAAATACTATTGCAATTCTCATTTTATTTTACCT	576				
Db	481	CCTGCCCTAGATTCGTAAATACTATTGCAATTCTCATTTTATTTTACCT	540				
Qy	577	TATATTTATGGATAAAAATTCTAAATCTTACTTACTTACTTACTTACTT	636				
Db	541	TATATTTATGGATAAAAATTCTAAATCTTACTTACTTACTTACTTACTT	600				
Qy	637	ATTTATATTATGGATAAAAATTCTAAATCTTACTTACTTACTTACTTACTT	696				
Db	601	ATTTATATTATGGATAAAAATTCTAAATCTTACTTACTTACTTACTTACTT	660				
Qy	697	TTGCGTTTCTTAATTAGTTAACTTCTTAAATTCTGATCGATT	756				
Db	661	TTGCGTTTCTTAATTAGTTAACTTCTTAAATTCTGATCGATT	720				
Qy	757	AGTGTGTGTCAAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG	816				
Db	721	AGTGTGTGTCAAAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG	780				
Qy	817	ATTTTCGATTAATTATGGATAATTCTTAAATTCTGATCGATT	876				
Db	781	ATTTTCGATTAATTCTTAAATTCTGATCGATT	840				
Qy	877	AATAATAATTCTTAAATTCTGATCGATT	936				
Db	841	AATAATAATTCTTAAATTCTGATCGATT	900				
Qy	937	CTTATACCATAATTAAATTCTGAGGACAAATTCTTAAATTCTGATCGATT	996				
Db	901	CTTATACCATAATTAAATTCTGAGGACAAATTCTTAAATTCTGATCGATT	960				
Qy	997	CATATTATAATTCTGATCTTCACTTCACTTCACTTCACTTCACTTCACT	1056	Qy	35	GTGCTGATATCTATGATTTGCAATTGCAATTGCACTTCTATCTATGCAAGAGCCCTG	94
Db	961	CATATTATAATTCTGATCTTCACTTCACTTCACTTCACTTCACTTCACT	1020	Db	421	GTACTGTAATCTGTA-TTTCGAGATGCAATTGCACTTCTATGCAAGAGCCCTG	363
Qy	1057	ATTTGAACTGTATAATTCTTAACTTCACTTCACTTCACTTCACTTCACT	1116	Qy	95	CAGAGGATCCAAATTAGTCTAAATTATCTGATCTGCAAACTGAGCCCCAA	154
Db	1021	ATTTGAACTGTATAATTCTTAACTTCACTTCACTTCACTTCACTTCACT	1080	Db	362	CAC-GATCCCAATTAGTCTAAATTATCTGATCTGCAAACTGAGCTGAG-CCTGA	306
Qy	1117	AGGCCAACGTCAGGTGTCAGAACACACTTGGTCAGTCATCAATTCCAGTA	1176	Qy	155	AACCGCTGTCGTCACTGCAGTCATCAATTCCAGTA	214
Db	1081	AGGCCAACGTCAGGTGTCAGAACACACTTGGTCAGTCATCAATTCCAGTA	1140	Db	305	AACCGCTGTCGTCACTGCAGTCATCAATTCCAGTA	247
Qy	1177	TGTTACGTTACTAAGGAATTCCAAATTCAATTCCAAATTTCGAGAAACG	1236	Qy	215	AGCTCTGTAACGGTGCATCTGATGCCAGATTGCAACTGTTATGTCAGGAACTCAAC	274
Db	1141	TGTTACGTTACTAAGGAATTCCAAATTTCGAGAAACG	1200	Db	246	AACCTGTAAGTGTCCCCTGATGTGAACTGTATGTCAGGAACTCAAC	187

Qy	275	TAACGGTAAAAATCCTCTGAACTTACCTTAGTAAATAATCACATAGCTCCAATCGTATC	334		VERSION	AY181254.1	GI:31322216
Db	186	TAACGGTAAAAATCCTCCAACTACTCTGAATTAAATCACATAGCTCAATCATTC	127	Gossypium hirsutum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvaceae; Malvoideae; Gossypium.	SOURCE		
Qy	335	CTCTAGTATATGAAATCACCCTTCGAATTGACCATGCGCTTGAGGATGAGAATCGAG	390	REFERENCE	1 (bases 1 to 598)	ORGANISM	
Db	126	TTCTGTGATATGAAATCACCCCTCTGAATTGACCATGCGCTGAGGATGAGAACAG	71	REPEATS	Taliercio, E.W. and Ulloa, M.	AUTHORS	
RESULT	4			TITLE	Gypsy element from cotton		
AF00583/c				JOURNAL	Unpublished		
LOCUS	AF00583	300 bp	DNA linear	PLN 17-DEC-2001	2 (bases 1 to 598)		
DEFINITION	Gossypium barbadense clone pXP030 repetitive DNA sequence.			AUTHORS	Taliercio, E.W. and Ulloa, M.		
ACCESSION	AF00583			TITLE	Direct Submission		
VERSION	AF00583.1			JOURNAL	Submitted (17-NOV-2002) USA-ARS, 141 Experiment Station Road, Stoneville, MS 38776, USA		
KEYWORDS				FEATURES	Location/Qualifiers		
SOURCE				Source	1. .598		
ORGANISM					/organism="Gossypium hirsutum" /mol_type="genomic DNA"		
					/cultivar="DES115"		
					/db_xref="taxon:3635"		
					<1. .5998		
					/note="contains nonfunctional gag protein, integrase, and reverse transcriptase due to mutation" </transposon="Gypsy retrotransposon"		
JOURNAL				ORIGIN			
MEDLINE				Query Match	12.5%	Score 179.4; DB 8;	Length 5998;
PUBMED	9582192			Best Local Similarity	70.4%	Pred. No. 8e-16;	
REFERENCE		(bases 1 to 300)		Matches	240; Conservat	Mismatches 101; Indels 0; Gaps 0;	
AUTHORS				Qy	42 ATATTATGATTTCGATTGCTAAAGCTCTATCATAGAAGAGCCCTGAGAGGA	101.	
TITLE				Db	5538 ATATCTCTCTTCAAGCTCTTGAAGCTCTTGTATTCGAGGTTGCTTCAGACGA	5419	
JOURNAL				Qy	102 TCCCBAATTAGTCAAAATTATTCGACTCTCGAAACGACTAGAGGCCAAACCCGT	161.	
FEATURES				Db	5478 TCAGCAATCACTTCATGCTGTTCAAGCTCAGAACAGTTAGGCCAAATCTCA	5419	
source				Qy	162 CGCTCACCCAACTGAGCTGCTAAATAACAGAGTATGACACTTATGACCTATGAGCCTCG	221.	
				Db	5418 CCTCTACATTAATGAACTCCACATAACAGAGCTAACACATAAAAGCCCTAG	5359	
				Qy	222 TAAGTGCCATCTGATGCGAGATGCGAGTATGCGAAACTGTTATGCGGAACCTAACAGGT	281	
				Db	5358 TAGGSGTGCCTAAATGAACTCTAGATGAGCTGTATTCTGAAACCGCAATGGC	5299	
				Qy	282 AAAAATCCCTCTCAACTCTTAAATCAATAGCTTCTCTCTCTCTCTAGT	341	
				Db	5298 AGGTGACTCGTCGCCAACTCCCTGAGCTTGTACACTGCTGAGATCTCTCTAG	5239	
				Qy	342 ATATGAAATCACCTCTCAATTGACCATGAGCTTGTACACTGCTGAGATCTCTAG	382	
				Db	5238 ATTGAAATACTCGTCGCCATCTCATAGCTGGGGTG	5198	
				RESULT	6		
				AF276939/c			
				LOCUS	AF276939	913 bp	DNA linear
				DEFINITION	Gossypium hirsutum retrotransposon Ty3-Gypsy-like nonfunctional integrase gene, partial sequence.		
				ACCESSION	AF276939		
				VERSION	AF276939.1	GI:2440674	
				KEYWORDS			
				SOURCE	Gossypium hirsutum (upland cotton)		
				ORGANISM	Gossypium hirsutum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvaceae; Malvoideae; Gossypium.		
RESULT	5			REFERENCE	1 (bases 1 to 913)		
AY181254/c				AUTHORS	Ulloa, M. and Meredith, W.R. Jr.		
LOCUS	AY181254	5998 bp	DNA linear	PLN 01-JUN-2003	TITLE	A Family of retrotransposon-like sequences associated with leaf	
DEFINITION	Gossypium hirsutum gypsy retrotransposon						
ACCESSION	AY181254						

JOURNAL	shape differences in cotton (Gossypium hirsutum L.)	FEATURES	Experiment Station Rd, Box 345, Stoneville, MS 38776, USA
REFERENCE	Unpublished	SOURCE	Location/Qualifiers
AUTHORS	2 (bases 1 to 913) Ulloa, M. and Meredith, W.R. Jr.		1. .927 /organism="Gossypium hirsutum"
TITLE	Direct Submission		/mol_type="genomic DNA"
JOURNAL	Submitted (10-JUN-2000) C. G. & P. Research Unit, USDA-ARS, 141		/db_xref="taxon:3635"
FEATURES	Experiment Station Rd, Box 345, Stoneville, MS 38776, USA		/clone="Cott-3"
SOURCE	1. .913 /organism="Gossypium hirsutum" /mol_type="genomic DNA" /db_xref="taxon:3635" /clone="Cott-2"		1. .927 /note="similar to reverse transcriptase sequence from Arabidopsis thaliana encoded by GenBank Accession Number AF077407" <!. .927 repeat_region /transposon="Ty3-Gypsy-like retrotransposon"
repeat_region	<1. .913 /note="similar to retrotransposon del 1-46 from Lilium henryi" /transposon="Ty3-Gypsy-like retrotransposon"	ORIGIN	
	<1. .635 /note="nonfunctional integrase due to mutation; putative zinc finger"	Query Match	Score 10.9%; Score 156.4%; DB 8; Length 927;
		Best Local Similarity	66.3%; Pred. No. 1..8e-12;
		Matches	0; Mismatches 121; Indels 1; Gaps 1;
		Qy	20 CGACGGCCGGCGGTGCTGATCATGATGTTAGATTGCTAGATTCCTATCT 79
		Db	363 CAAACTCCCCATAGAGATTCACTCTTCTAGTCCAAATTGGCTATGACTCTGTT 304
		Qy	80 ATCAGAGAGCCCTGAGAGATCCAATTAGCTAAATTATCTTCACTCTCGAAC 139
		Db	303 GTCAAGATGCTTCTCAATTAGTTGCAATCAGTTTACCTTCTCTAGTTATGAGAAC 244
		Qy	140 CAACTCAGGACCCAAACCGCTCGGTACCCAACTTCAGTCTAAATAACGAGATGACA 199
		Db	243 TAACCTCTGGCCCGAGACTGCCCTTGCTTAGCTCAGTCAAAGGTAGAGTACGACA 184
		Qy	200 CTTATGACCATAAGGCCCTCGTAAGGTGCCATCTAGATGCCAGATGGAAACGTATT 259
		Db	183 CCTTGACCATAACGCCCTCGTAAGGTGCCATTGAACTACTAGTGGCTAGTATT 124
		Qy	42 ATATCTATGATTTCAGATTGCTATAGAACCTCTATCATGAAAGACGCCTGAGAGGA 101
		Db	340 ATATCTTCTCTTCAAGTCTGCTATAGACTTGTATTGGAGGTGTGGTTAGAGGA 281
		Qy	102 TCCCCAATTAGCTAAATTATCTCTGCTCGGAAACCAACTCAGGACCCAAACCGT 161
		Db	280 TCACGAACTCACCTTCATGGTTCTCGTCCTCGGAAACCAACTTACCTAAC 221
		Qy	162 CGCTCACCCAACTCAGCTAAATAACAGATGAACTATGACCATAAGGCCCTCG 221
		Db	220 CTTTCACTTAATTCATCCAACTAACATACAGACTACGAGCTAAC 161
		Qy	222 TAAGGTCCCATCTAGATGCCAGATGGAAACTCTGTTAGCTAACCTACGGT 281
		Db	160 TAGGGTCCAAATTGAAACTAGATTGAACTGTTATGTATGCACTAGCCATGGC 101
		Qy	282 AAAAATCTCTCAACTACCTCTAGATAATAAATCACATAGCTCCAATCTGATCCCTAGT 341
		Db	100 AGGTACTCGTCCCACACTCCCTGAACCTCATCAAACTTCGGACATCCCTAAAG 41
		Qy	342 ATATGATCACCTCACCTGAAATTGACCATGGCTCTGAG 380
		Db	40 ATTGATAACTCGTCCCACACTCCCTGAACCTCATCAAACTTCGGACATCCCTAAAG 2
		RESULT	8
		LOCUS	AC146584
		DEFINITION	Medicago truncatula clone mth2-68k18, WORKING DRAFT SEQUENCE, 6 ordered pieces.
		ACCESSION	AC146584
		VERSION	AC146584_28 GI:52219258 HTGS_DRAFT.
		KEYWORD	Medicago truncatula (barrel medic)
		ORGANISM	Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicots; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
		REFERENCE	1 (bases 1 to 111063)
		AUTHORS	Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D., and Roe, B.A.
		TITLE	Title Unpublished
		JOURNAL	2 (bases 1 to 111063)
		REFERENCE	Lin, S., Dixon, R., May, G., Sumner, L., Gonzales, B., Cook, D., Kim, D., and Roe, B.A.
		AUTHORS	Title Direct Submission
		TITLE	Title Submitted (04-SEP-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
		JOURNAL	

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1	79253: contig of 79253 bp in length
	79353: gap of unknown length
2	79354: contig of 12686 bp in length
	92039: gap of unknown length
3	92139: contig of 29118 bp in length
	92140: gap of unknown length
4	92140: contig of 121257 bp in length

Query Match	9.6%;	Score 137.6;	DB 2;	Length 78069;		ORIGIN
Best Local Similarity	57.8%;	Pred. No. 2.8e-10;				
Matches 245;	Conservative 0;	Mismatches 179;	Indels 0;	Gaps 0;		
Qy	27 CGGGCTGGTGTGATCATGATTGATAAGCTTGTCAAGAACTCTATCATGAA 86					
Db	29516 CCTTCCTGAAACTCAGATCTTCTACGCTTATCATGAACTCTTGTGATTCTGC 29457					
Qy	87 GAGCCCTGAGGGTCCAAATTACTCTAAATTCTCAGTCAGTCTCGGAACCAACTCA 146					
Db	29456 GAGGCCCTCATTTTCAGTCTCGAAGCTTCTAGTAGCTGTGAACTCTCT 29397					
Qy	147 GGACCCAAAACCGTGGTCAACCCAACTTCAGTCTAAATATAACAGATGATCACCTATCA 206					
Db	29396 GATCCCTAAGGCAACACTCTACCTCTACCTCAACACCACACGGGTTCTCGCATCTCGA 29337					
Qy	207 CCATATAGGCTCGTAAGGTGCCATCTAGATGCCAACACTGTTATTGTAGGCG 266					
Db	29336 CCATATAGGCTCGAACGGTCCATACTGAAAGTAACTATTTGATGTGTG 29277					
Qy	267 AACTCAACTAACGGTAAAAAATCTCTCAACTACCTTGTAAATAATCACATGCTCAA 326					
Db	29276 AACCTCATCAAGGAGATGAGTCAAGTCTCTGCTCAAGAACAAATTCTC 29217					
Qy	327 ATCGTATCCCTCTAGTATGATGATCACTCCAAATTGACATCGTCTCGAGGTGGAA 386					
Db	29216 AACAAATTCTCTAGCCTAGTCACTGGATTCCTCTCCAACTGACCATCTGTCTCGGATGATAC 29157					
Qy	387 GCAGACGGTCCACGGATTACTAAATGGTACCTATAAAATTATTATTTTAAAAA 446					
Db	29156 GCGGAACCTCAACCTCAACTCTGAACCTCGAACCTCTTGCACAACTCTTCAAAATCTAGAA 29097					
Qy	447 TTGA 450					RESULT 14 AC149299
Db	29096 TTAA 29093					LOCUS AC149299 143392 bp DNA linear PLN 02-JUN-2004 DEFINITION Populus balsamifera subsp. trichocarpa clone Popl-037B22, complete sequence. ACCESSION AC149299 VERSION 1 KEYWORDS HTG.
Qy						SOURCE Populus balsamifera subsp. trichocarpa (Populus trichocarpa) ORGANISM Populus balsamifera subsp. trichocarpa DEFINITION Unpublished REFERENCE AC149299_1 GI:47900639 AUTHORS Stanford Human Genome Center. CONTRIB DOE Joint Genome Institute and Stanford Human Genome Center. TITLE Direct Submission JOURNAL Submitted (02-JUN-2004) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA COMMENT Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www-Bhrc.stanford.edu FEATURES Quality Phrap Quality >=40 100% of Sequence; Source /organism="Populus balsamifera subsp. trichocarpa" /mol_type="genomic DNA" /sub_species="trichocarpa" /db_xref="taxon:3604" /clone="Popl-037B22"
Qy						ORIGIN Query Match 9.6%; Score 137.2; DB 8; Length 143392; Best Local Similarity 62.0%; Pred. No. 2.8e-10; Matches 217; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 38 CTTGATATCTATGATTTCAGATTGATAAGACTCTATCATAGAAGACGCCCTGGAG 97
 Db 108298 CTCPAAGTCAAGCATTCTCTATCTCGCGAACTCTTGTCTACTCTGCTGTTGAG 108357
 QY 98 AGGATCCAAATTAGTCATAATTATCTTCAGTCCTGGAAACCACTAGGACCCAAAC 157
 Db 108358 CTTCTTTCTATTACCTCTATCTCTGAGTAATCTGATACTCTGGTCCCATAG 108417
 QY 158 CGCTGGCTCACTCAACTCTGCTATAATAACAGAGTTAACCTATGAGGC 217
 Db 108418 CCTCTCTCCTACCAACCTCAACCCAAACCAACCGGATCTAACCTCCACAAAGC 108477
 QY 218 CTCGTAAGTGCCATCTAGTGCCTAGATGCTAGTGGAACTCAACTAA 277
 Db 108478 CTCTAAAGTGGCCATTCTATGCTGATAACTGTTGTTGAAAGGAAATTCCACTAA 108537
 QY 278 CGGTAAAATTCCTCTCAACTCCATTGATAATAATCATAGTCCTCAAATGTTATCCTC 337
 Db 108538 TGGTAGGAACTTACTCCAACTCCAACTCCAAATCCCTAACATATCCT 108597
 QY 338 TAGPATATGATCACCTCTCAATTGACCATGCTTGGGTTGAATG 387
 Db 108598 CAAGATCTGATAGTCCTCAGACTCGTACATGAAAG 108647

RESULT 15
 AC146794/C
 LOCUS AC146794
 DEFINITION Medicago truncatula clone mth2-1019, WORKING DRAFT SEQUENCE, 11
 * unorderd pieces.
 ACCESION AC146794
 VERSION GI:50345165
 KEYWORDS HTGS DRAFT
 * SOURCE Medicago truncatula (barrel medic)
 HTGS: Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eu dicots; core eudicots;
 rosids; euroids I; Fabales; Fabaceae; Papilionoidae; Trifolieae;
 Medicago.
 1 (bases 1 to 107287)
 Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
 and Roe,B.A.
 Unpublished
 REFERENCE Submitted 107-OCR-2003) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 3 (bases 1 to 107287)
 Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B., Cook,D., Kim,D.
 and Roe,B.A.
 Direct Submission
 Submitted 14-SEP-2004) Department Of Chemistry And Biochemistry,
 The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 On Jul 16, 2004 this sequence version replaced gi:50057955.
 COMMENT ----- Genome Center
 Center: Department Of Chemistry And Biochemistry
 The University Of Oklahoma
 Center code:OKNOR

Query Match 9.5%; Score 136.4 - DB 2; Length 107287;
 Best Local Similarity 61.0%; Prod. No. 3.9e-10;
 Matches 221; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 45 TCTATGATTTCAGATTGCTATAGACTCTATCTATCAAGAGCGCTGCAAGGGATCC 104
 Db 84701 TCTTCCATGTCGTTGATCTATGTTGACTCTGCACTTCATCTTTCT 84542
 QY 105 CAAATTAGCTAAATTATCTCTCGTCTGGAAACCAACTCTGAGGACCCAAAACCGTCSC 164
 Db 84641 CTTTAAATGCTTAACTCTCTGTPATCTGTAATTCGTTGACAATATTCTGCACTACACTC 84582
 QY 165 TCACCCAACCTGCTTAATAAACAGATGACTATGACCATATGAGCTATGAGCTTCGTA 224
 Db 84581 TCACCCGACTCAAAACCACATACAGACTCTGGACCTTCGACATAGCTTCGAAT 84522
 QY 225 GGTCGCATCTGATGCCAGATGGAAACTCTGTTATGTTAGCGGAACTCAACTAAAGGTAA 284
 Db 84521 GGTCGATTCCTATGAGTGTAACTGAGATGTTGACTGTGAACTCTGAACTGGTACA 84462
 QY 285 AAACTCTCCTCAACTAACCTTCTGTTAGTAAATCACATAGCTCCAAATGTTCTCTAGTATA 344
 Db 84461 TGACTATCCCAGTCCCACTTGATCAAGTCAACTCTCACAAATCTCAACGAC 84402
 QY 345 TGAATCACCTCTCTCAATGACCATGCTGTTGAGATGAAATGGAGCTGCTGACCGA 404
 Db 84401 TGAATCTGCTCTCTGACTGACCTCTGTTGCGATGATAAGCGAACTCAACCTCAAC 84342
 QY 405 TT 406
 Db 84341 TT 84340

Search completed: August 13, 2005, 11:00:00
 Job time : 10343 secs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 2068: contig of 2068 bp in length

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 13, 2005, 02:09:43 ; search time 7384 Seconds
(without alignments)

Title: US-10-089-543-2
Perfect score: 1433
Sequence: 1 actataggccacgcgtggc.....tgagagaatccatcacatc 1433

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3429544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : EST:
1: 9b_est1:
2: 9b_est2:
3: 9b_hrc:
4: 9b_est3:
5: 9b_est4:
6: 9b_est5:
7: 9b_est6:
8: 9b_gbs1:
9: 9b_gbs2:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	24.4	15.7	581	9 CL864797	CL864797 TM1-GSS00
c 2	181.8	12.8	768	9 CL251651	CL251651 2NMBBD060
c 3	175.4	12.2	758	9 CL404830	CL404830 2NMBBD039
c 4	172.8	12.1	1006	9 CL263790	CL263790 2NMBBD062
c 5	172	12.0	447	9 CL864019	CL864019 TM1-GSS00
c 6	164.6	11.5	973	9 CL249359	CL249359 2NMBBD059
c 7	162.4	11.3	762	9 CL863878	CL863878 TM1-GSS00
c 8	157.6	11.0	643	9 CL864239	CL864239 TM1-GSS00
c 9	155.8	10.9	355	9 CL202255	CL202255 2NMBBD056
c 10	151.6	10.6	1057	9 CL285168	CL285168 2NMBBD062
c 11	147.4	10.3	957	9 CL291015	CL291015 2NMBBD063
c 12	146.4	10.2	739	9 CL864139	CL864139 TM1-GSS00
c 13	143.2	10.0	569	8 BH021651	BH021651 GH MBDB000
c 14	142	9.9	686	8 BH022375	BH022375 GH MBDB000
c 15	133.8	9.8	725	9 CC746178	CC746178 2NMBBD012
c 16	133.8	9.8	781	8 BH022660	BH022660 GH MBDB000
c 17	139.6	9.7	705	9 CC688457	CC688457 OGWCBS37TH
c 18	139.6	9.7	1015	9 CL010422	CL010422 2NMBBD055
c 19	137.4	9.6	509	4 BI122809	BI122809 1013P31P
c 20	137.4	9.6	799	8 BZ702320	BZ702320 PUD182TD
c 21	137.2	9.6	660	8 BH021854	BH021854 GH MBDB000
c 22	137	9.6	694	8 BZ420292	BZ420292 IF66d04.b
c 23	136.8	9.5	697	8 BH885303	BH885303 osi16d03
c 24	136.8	9.5	843	9 CG006002	ZURCL81TV

ALIGNMENTS

RESULT	1	CL864797	581 bp DNA linear	GSS 19-AUG-2004
LOCUS	TM1-GSS000073r	BAC and BIBAC libraries from Upland cotton Genetic standard TM1. Goosypium hirsutum genomic clone GH-TM1-CBV149b20 5',		
DEFINITION		Genomic survey sequence.		
CL864797				
ACCESSION	CL864797.1	GI:51321527		
VERSION	C 40	135.2	9.4	848 9 CG245637
KEYWORDS	C 41	134.8	9.4	857 9 CG909847
SOURCE	C 42	134.8	9.4	651 8 B2488595
ORGANISM	C 37	135.2	9.4	653 9 CC760866
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Goosypium.	C 38	135.2	9.4	B2457826
REFERENCE	C 39	135.2	9.4	B2457826 BONLID23TP
AUTHORS	C 40	135.2	9.4	B2453701 BONF55TF
Xu, Z., Kohel, R.J., Zhang, H.B., Dong, J.J., Covaleda, L., Lee, M., Koo, P. and Yu, J.Z.	C 41	134.8	9.4	BZ719317 PUCPH5STD
TITLE	C 42	134.8	9.4	CG861526 2NMBBD035
JOURNAL	C 43	134.8	9.4	CG603679 OGWEBS-18TV
COMMENT	C 44	134.6	9.4	CG300841 OGOC05TV
OTHER_GSSS:	C 45	134.2	9.4	CC145564 2NMBBD000

FEATURES	Location/Qualifiers	High quality sequence stop: 581.
SOURCE		1. - 581
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		/tissue="Young leaves"
		/lab_host="DH10B"
		/clone_lib="BAC and BIBAC libraries from Upland cotton
		genetic standard TM-1"
		/vector="pCR2.1"
		/db_xref="taxon:3635"
		/clone="GH-TM1-CBV149b20"
		for more details on
		library construction, ordering clones and sequence
		analysis see
		http://algodon.tamu.edu/htdocs-cotton/cottontdb.html

Query Match	12.2%	Score 175.4; DB 9; Length 758;	Qy	36	TGCTTGATATCTAGATTTCAGATTGGATAAGACTCTATCATTAGAGAGCCCTGC 95
Best Local Similarity	75.1%	Pred. No. 3.6e-19;		Db	96 TACCTAATCTCTTGGCATTTAGGTCCGGTAGACTGCTTCACTGCTTCCTTC 155
Matches 259; Conservative 0; Mismatches 81; Indels 5; Gaps 3;					
Qy	52	TTTTCAGATTGATAGA GACTCTATCATCGAGAGCGCTGAGAGGATCCAAATA 111	Qy	96	AGAGGAATCCGAATTAGTCCTAAATTATCTCAGTCGGAAACCTGAGGCCAAA 155
Db	750	TATTCGAATTGATAGA TTTCGTCATATCGAGCGCTTTCAAACGATTCCGAATCA 692	Db	156	AGTGGTGTCTGAATCAGTTTACCTTCTTCGGTATCAGAACTTAACCTGGCCCTAGA 215
Qy	112	GTC TAA AAT ATTATCCTCGT CCG GAA ACC AAC TCG AGA CCC AAACCCGTCACCCA 171	Qy	156	ACCCGTCACCCAACTCAGTCCTAATAAACGAGTATGACCTTATGACCATATAAC 215
Db	691	ATCTAATCTCATCCCTCATCTCAGAACCTCGGACCAACTCGGACCTGGCC 632	Db	216	ACCTCTGCTGCCAACCTAGTCCTAACGGTAGACGACATAGCCATAAC 275
Qy	172	ACTCAGT-CPAATATAAACAGAGTATGACCATATAGGCCCTGTAAGGTGCC 230	Qy	216	GCCTGTAAGGTGCCATCTAGATGCCAGATGGAAACGTTATGAGCTAACCT 275
Db	631	ACTTACTCCCACCGTCAAGGAGTGGCACCTAACCGTACAGTCCTGAAGGTGCC 572	Db	276	GCCTGTAAGGTGCCATTAGTGAATCTGGTGGCTATTATAAGGGAACCTCTACT 335
Qy	231	ATCTAGATGCCAGATTGAAACTCAACTAACGTTATGACCATATAGGCCCTGTAAGGTGCC	Qy	276	AACGTTAAAAATCTCTCACTACCTTGTAAATTAATCAC-AATGCTCAAATGTATC 334
Db	571	ATCTGGATGCTGAGCTGGAACTCTCTGCTAAACTCTGCTAA--TGACAAGTAC 515	Db	336	AGCGCCAAATAGTCTCCAGGTCGGAATTCATGCTTCTAACATATC 395
Qy	291	TCTCAACTACCTTAGTAAATCATACATAGCTCCAAATCTCTAGTATGATGATC 350	Qy	335	CTCAGTATGATGATCACCTCACCTCAATGCTTCACTGTCCTCGATCTGAATC 390
Db	514	TCCCAACTACATCAGAAATCATAAATCATACATCTCCAACTGTCCTCGATCTGAATC 455	Db	396	CTCCATATTGATCTCCTCTGATGACCACCTATCTGGATGAPACGGAG 451
Qy	351	ACCTCTCAAATTGACCATCGGTCTGAGGATGGAATCGAGACCGG 395			
Db	454	ATCCCTCTCACTGACCGCTGTTGAGGAAAAACGACTACTG 410			
			RESULT 5		
			CL864019/c		
			LOCUS	CL864019	447 bp DNA linear GSS 19-AUG-2004
RESULT 4			DEFINITION	TM1-GSS00206f	BAC and BIBAC libraries from Upland cotton genetic standard TM-1. Gossypium hirsutum genomic clone GH-TM1-CBY047P09 5', genomic survey sequence.
CL263790			ACCESSION	CL864019	
DEFINITION	ZMMBBB06223P14f ZMMBBB (HindiII) zea mayes genomic clone		VERSION	GI:51320749	
REFERENCE	ZMMBBB06223P14 5', genomic survey sequence.		KEYWORDS	GSS.	
VERSION	CL263790		SOURCE	Gossypium hirsutum (upland cotton)	
KEYWORDS	CL263790.1 GI:41627929		ORGANISM	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; core eudicots; rosids; euroids II; Malvales; Malvaceae; Malvoideae; Gossypium.	
- SOURCE	zea mayes		REFERENCE	Xu, Z., Kohel, R.J., Zhang, H.B., Dong, J.J., Covaleda, L., Lee, M., Koo, P., and Yu, J.Z.	
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACAD clade; Panicoideae; Andropogoneae; Zea.		AUTHORS	Unpublished (2004)	
	1 (bases 1 to 1006)		TITLE	Other GSS: TM1-GSS00206r	
REFERENCE	Bharti, A.K., Young, S., Keizer, G., Bronzino, A.C., Zohner, V., Fuks, G., Yu, Y., Wind, R. and Messing, J.		JOURNAL	Contact: John Z. Yu	
VERSION	Unpublished (2003)		COMMENT	cotton Molecular Genetics Laboratory	
KEYWORDS	Sequencing of the maize genome at PGIR (2003c)			USDA-ARS Crop Germplasm Research Unit	
- SOURCE	CONTACT: Bharti, A.K.			2765 FAB Road, Building 11, College Station, TX 77845. USA	
ORGANISM	Dr. Joachim Messing's lab			Tel: 979-260-9237	
	The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University			Fax: 979-260-9333	
	190 Frelinghuysen Road, Piscataway, NJ 08854, USA			Email: zyu@quitun.tamu.edu	
	Tel: 732 445 3801			for more detail, please see	
	Fax: 732 445 5735			http://algodon.tamu.edu/htdocs-cotton/cottondb.html	
	Email: bharti@waksman.rutgers.edu			Seq primer: gp010	
	Seq primer: T7			Class: BAC ends	
	Class: BAC ends			High quality sequence stop: 447.	
	High quality sequence start: 51.			Location/Qualifiers	
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	/cultivar="B73"			/cultivar="TM-1"	
	/db_xref="taxon:4577"			/db_xref="taxon:3635"	
	/clone="ZMMBBB0623P14"			/clone="GH-TM1-CBY047P09"	
	/lab_host="E. coli DH10B"			/lab_host="DH10B"	
	/clone_lib="ZMMBBB (HindiII)"			/clone_lib="BAC and BTBAC libraries from Upland cotton	
	/note="Vector: pCLD0451; pheloBAC11; For more details on library construction, ordering clones and sequence analysis see http://algodon.tamu.edu/htdocs-cotton/cottondb.html "			genetic standard TM-1"	
ORIGIN				/note="vector: pCLD0451;"	
Query Match	12.1%	Score 172.8; DB 9; Length 1006;			
Best Local Similarity	69.7%	Pred. No. 9.2e-19;			
Matches 248; Conservative 0; Mismatches 107; Indels 1; Gaps 1;					

ORIGIN

Query Match 12.0%; Score 172; DB 9; Length 447;
Best Local Similarity 67.7%; Pred. No. 1.4e-18;
Matches 241; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 35 GTGCTTGATATGTTTCAGATTGATAAGACTCTATCATCGAAAGACGCCCTG 94
Db 417 GTATTCATATCCTTACGGCTTCAGATCTGCATAGCACTTTGCCTATCGACGTTCCCT 358
QY 95 CAGAGGATCCGAATTAGTCTAAATTATCTCACTCTCGAAACCACTAGACCCA 154
Db 357 TAATCCATCTCAATAACCTGACCTTATCTCGACCTAACATCGCATTCAG 298
QY 155 AACCGCTCGTCACTCAACTCAGTCCTAATAACGAGATGACACTATGACCATATAG 214
Db 297 AACCTCTGCCTCCCCAGTTAGTCACACTAGCTGTTGACACTACAGTCAG 238
QY 215 AGCCCTGTAGGTGCCATTAGATGCCAGATGGCAACTCTAAC 274
Db 237 TGCTTCATAAGGTGCCATTAGCTGCAATACTGGACTTAACATTGGTGTATGCCAAACTCTC 178
QY 275 TAACGTTAAAATCCTCTCAACTACCTCTAGTAAATACTACATACTGGTCAATGTATC 334
Db 177 CAAAGGCAAGTAGTCTCCCAACTACCTCTGGAAATCATAAACACATCCCTCAGCATTC 118
QY 335 CTCTGATATGAAATCCCTCTCAAATTGACCATCTGGCTGAGGATGGATGCAAG 390
Db 117 TCCAGATCTGAATAACTCTTCCGACCATCTGGATGAAAGCGC 62

RESULT 6

CL249359/c CL249359 973 bp DNA linear GSS 22-JAN-2004
LOCUS ZMMBBB0595C21F ZMMBBB0595C21 5', Genomic survey sequence.
DEFINITION Zea mays genomic clone
ACCESSION CL249359
VERSION 1 GI:41105913
KEYWORDS GSS.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Poaceae; PACCAD clade; Panicoidea; Andropogoneae; Zea.
REFERENCE Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohner, V.V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
AUTHORS Unpublished (2003)
TITLE Contact: Bharti, A.K.
COMMENT Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq. primer: T7
Class: BAC ends
High quality sequence start: 50.

FEATURES

source 1..973
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/cuiElivar="B73"
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/note="Vector: pCUG1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 11.5%; Score 164.6; DB 9; Length 973;

Best Local Similarity 65.8%; Pred. No. 2.1e-17;
Matches 239; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 28 CGCCTGCTGTCAGATCTATGTTTCAGATTGCTATCTATCATCGAG 87
Db 865 CGACTTGGAACTCATATCCTTGCCTTAAGTCATGATTCATGAG 806
QY 88 ACGCTTGAGGATTCGCCAAATTAGTCCTAATTCCTCACCTCTCGAAACCAACTCAG 147
Db 805 CTCCTTCAAACTATCTGGATCATCTTCACCTTCCTCAGTCATGATTCATGAG 746
QY 148 GACCCAAACCCGCGTCACCACTCGATCTAAACAGATGACACTTGTAC 207
Db 745 CCCGCATATCTTTCTCAGCTGCTAGTCATGATTAATAGTCGACATGAC 686
QY 208 CATAGAGCCCTGCTTAAGCTGCCATTAGTCAGATGCCAGATTGGCA 267
Db 685 CATAATAACCTCTAGTCATGTCGTGCTTCATGCTGACATTAATAGTCGACATGTC 626
QY 268 ACTGACTAACGTTAAATAATCACATAGCTCCAAA 327
Db 625 ATTTGACCATGTTAAATTATTCCTCCAGTTAACCTGATCACACATTGAA 566
QY 328 TCTGATCTCTAGTATGAACTACCTCTCAATTTGACCATGGCTGAGGATGGAAATG 387
Db 565 GCATATCTCGAGATTGAACTGAACTGCTGAGCTGACCTCAAC 506
QY 388 CAG 390
Db 505 TAG 503

RESULT 7

CL863878 CL863878 762 bp DNA linear GSS 19-AUG-2004
LOCUS TM1-GSS000151F BAC and BAC Libraries from Upland cotton Genetic DEFINITION standard TM-1 Gossypium hirsutum genomic clone GH-TM1-CIV026005 5', genomic survey sequence.
ACCESSION CL863878
VERSION CL863878.1 GI:51320608
KEYWORDS GSS.
SOURCE Gossypium hirsutum (upland cotton)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicots; Poaceae; PACCAD
Keywords: eurosids II; Malvaceae; Malvoideae; Gossypium.
REFERENCE Xu, Z., Xiong, R.J., Zhang, H.B., Dong, J., Covaleda, L., Lee, M., Koo, P.
AUTHORS and Yu, J.Z.
TITLE Genome-Wide Synteny between Arabidopsis and Cotton COMMENT unpublished (2004)
Other GSS: TM1-GSS000151r
Contact: John Z. Yu
Cotton Molecular Genetics Laboratory,
USDA-ARS Crop Germplasm Research Unit
2765 FAB Road, Building 11, College Station, TX 77845. USA
Tel: 979-260-9337
Fax: 979-260-9333
Email: zyu@utun.tamu.edu
For more detail, please see
<http://algodon.tamu.edu/hdocs-cotton/cottondb.html>
Seq. primer: sp010
Class: BAC ends
High quality sequence stop: 762.
FEATURES
Source 1..762
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/clone="ZMBBB0595C21"
/lab_host="E. coli DH10B"
/note="Vector: pCUG1; Site_1: HindIII; Site_2: HindIII"
/issue type="young_leaves"
/lab_host="DH10B"

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genetic standard TM-1"
/note="Vector: pCIN4541; pBeloBAC11; For more details on
library construction, ordering clones and sequence
analysis see
<http://algodon.tamu.edu/htdocs-cotton/cottontdb.html>"

ORIGIN

Query Match 11.3%; Score 162.4; DB 9; Length 762;
Best Local Similarity 65.4%; Pred. No. 5e-17;
Matches 238; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

Qy 27 CGGGGCGGTGCTTGATATTGATGTTGATAGACTTCTATCTATCGAA 86
Db 153 CCCATCTGATACTCAATATCCTCTTCATGGCATAGACTCTG 212

Qy 87 GAGGCCGAGGGATCCAAATTAGCTAAATPATCTCTAGCTCGGAACCACTCA 146
Db 213 GCTGCCTCTGAGCTTCAAGCTTCAAGGTTACTCTCTGCTAGCATTC 272

Qy 147 GSACCCAAAACCGGTGCTCACCCAACCTCAGCTCTAAATACAGAGTATGACACTTGA 206
Db 273 ACTCCAAAATTAACTTCACTTCACCGAGCTGGTCAAAACATGGCTACGCAATTGGCA 332

Qy 207 CCATATGAGCTCTGTAAGGGCCATCTAGATGCCGATTTGAAACTGTTATGGGGC 266
Db 333 CGGTACAAAGCTTCCPAAAGGTGCCATTAACTCTGATTTGTAAGGCA 392

Qy 267 AACTCACTAACCGTAaaaaATCCTCTCAACTAACCTAACATAGETCTCAA 326
Db 393 ATTCACTCAAGGTAATAACGGTTCCCATGAACCACTAACTCAGGATCAGCATCTC 452

Qy 327 ATCGTATCTCTAGTATGATGATCACTCTTCACAAATTGACCATGTTGGGGATGAAAT 386
Db 453 AACATATCCTCAAGTAGTACCGTTCCATGAACCACTAACTCAGGATCAGCATCTC 512

Qy 387 GCAG 390
Db 513 GCAG 516

*4

RESULT 8
CL864239
LOCUS TM1-GSS000337f
DEFINITION BAC and BIBAC libraries from Upland cotton genetic
standard TM-1 Gossypium hirsutum genomic clone GH-TM1-CBV088C22 5' ,
Genomic survey sequence.
CL864239
VERSION CL864239_1 GI:51320969
GSS.

ORGANISM Gossypium hirsutum (upland cotton)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 643)
Xu, Z., Kohel, R.J., Zhang, H.B., Dong, J., Covaleda, L., Lee, M., Koo, P.,
and Yu, J.Z.
TITLE Genome-Wide Synteny between *Arabidopsis* and Cotton
COMMENT Unpublished (2004)
Contact: John Z. Yu
Cotton Molecular Genetics Laboratory
USDA ARS Crop Germplasm Research Unit
2765 F&B Road, Building 11, College Station, TX 77845, USA
Tel: 979-960-9237
Fax: 979-960-9333
Email: zyu@quitun.tamu.edu
for more detail, please see
<http://algodon.tamu.edu/htdocs-cotton/cottontdb.html>

Seq primer: sp010
Class: BAC ends

High quality sequence stop: 643.

	FEATURES	Source	Location/Qualifiers
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			2. 11.0%; Score 157.6; DB 9; Length 643; Best Local Similarity 64.6%; Pred. No. 3.1e-16; Matches 235; Conservative 0; Mismatches 129; Indels 0; Gaps 0;
			3. 27 CCGGCTGGCTGCTGATATCTATGATTTCGATTTGCAATTGCTATCTATGAA 86 Db 146 CCCACCTGATACTTATGCTTCTGTTCAATTGCGTACGACTCTGAGATCTGTG 205
			4. 87 GACGCCGAGGATCCAAATTAGTCTAAATTATCTGTTAAATTATCTGCTTCGGAAACCACTCA 146 Db 206 GCTGCCTTCAGACTCTTACGGATTTACTCTTACTCTGTTCAATTAAATCA 265
			5. 147 GGACCCAAAACCGGTGCTCACCCAACTCAGTCTAAATAACAGGATGACCTATGAA 206 Db 266 ACTTCGAAAATTATTTACTTTGCGGACTCTGTTACGGCATTTACGCA 325
			6. 207 CCATATGAGCTCTGTAAGGGCCATCTAGATGCCGATTTGAAACTGTTATGGGGC 266 Db 326 CGGTGAAAGCTCTGTAAGGTGCACTTGTGCTGAGCTGGCTCAAAACATGTTACGGCATTTACGCA 385
			7. 207 CCATATGAGCTCTGTAAGGGCCATCTAGATGCCGATTTGAAACTGTTATGGGGC 266 Db 386 AATTCAATCAAGGTAATAACCGGCTCAAGTGTGCAATTGCGGACTCTGAGGATTCAGATCTC 445
			8. 327 ATCGTATCTCTAGTATGATGATCACTCTTCACAAATTGACCATGTTGGGGATGAAAT 386 Db 446 AACATCACCTCTCAAGSTATCTGATATGTTGACATTCAGTGAATACTTGTGTAAGGCG 385
			9. 387 GCAG 390 Db 506 GCGG 509

RESULT	9	CL202255/C
CL864239		LOCUS CL202255
DEFINITION		ZMMBBb0563L12r ZMMBBB (HindIII) zea mayes genomic clone
REFERENCE		ZMMBBb0563L12 3', genomic survey sequence.
AUTHORS		ACCESSION CL202255
JOURNAL		VERSION CL202255..1 GI:40718214
COMMENT		KEYWORDS GSS .
		SOURCE Zea mayes
		ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
		Spermatophyta; Magnoliophyta; eu dicots; core eudicots;
		clade; Panicoidea; Andropogoneae; Zea.
		REFERENCE 1 (bases 1 to 355)
		AUTHORS Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohovetz, V., Fukasawa, Y., Wing, R. and Messing, J.
		TITLE Title Sequencing of the maize genome at PGIR (2003c)
		JOURNAL Unpublished (2003)
		COMMENT Contact: Bharti, A.K.
		Dr Joachim Messing's lab The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
		190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 180.
 Location/Qualifiers
 1. .355

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/mol_type="genomic DNA"
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/db_xref="taxon:4577"
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/lab_host="E. coli DH10B"
/clone_lib="ZMBB (HindIII)"
/note="Vector: pcUGI; Site_1: HindIII; Site_2: HindIII"

FEATURES
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Db	0	42	155.8	9	1	355
Qy	157	217	155.8	9	1	355
Db	295	217	155.8	9	1	355
Qy	277	235	155.8	9	1	355
Qy	337	235	155.8	9	1	355
Db	175	175	155.8	9	1	355

ORIGIN

Query	Match	Length	Score	DB	Start	End
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Qy	68.3%	239	151.6	9	1	239
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Db	138	138	151.6	9	1	138
Qy	102	197	151.6	9	1	197
Qy	162	198	151.6	9	1	198
Db	198	257	151.6	9	1	257
Qy	222	258	151.6	9	1	258
Db	282	318	151.6	9	1	318
Qy	342	378	151.6	9	1	378
Db	390	427	151.6	9	1	427

RESULT 11
 CL291015/C
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 DEFINITION ZMBB (HindIII) Zea mays genomic clone
 /note="genomic survey sequence."
 ACCESSION CL291015
 VERSION CL291015.1
 KEYWORDS GI:42505402
 SOURCE GSS
 ORGANISM Zea mays
 REFERENCES 1 (bases 1 to 957)
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 TITLE Sequencing of the maize genome at PGIR (2003c)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Bharti,A.K.
 Dr.Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 405.
 Location/Qualifiers
 1..1057

FEATURES
 source

Query	Match	Length	Score	DB	Start	End
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Qy	68.3%	239	151.6	9	1	239
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Db	138	138	151.6	9	1	138
Qy	102	197	151.6	9	1	197
Qy	162	198	151.6	9	1	198
Db	198	257	151.6	9	1	257
Qy	222	258	151.6	9	1	258
Db	282	318	151.6	9	1	318
Qy	342	378	151.6	9	1	378
Db	390	427	151.6	9	1	427

RESULT 12
 CL285168 1057 bp DNA linear GSS 10-FEB-2004
 DEFINITION ZMBB (HindIII) Zea mays genomic clone
 /note="genomic survey sequence."
 ACCESSION CL285168
 VERSION CL285168.1
 KEYWORDS GI:42499555
 SOURCE GSS
 ORGANISM Zea mays
 REFERENCES 1 (bases 1 to 1057)
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 TITLE Sequencing of the maize genome at PGIR (2003c)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Bharti,A.K.
 Dr.Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 405.
 Location/Qualifiers
 1..1057

FEATURES
 source

Query	Match	Length	Score	DB	Start	End
Qy	10.6%	161	151.6	9	1	161
Qy	68.3%	239	151.6	9	1	239
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Db	138	138	151.6	9	1	138
Qy	102	197	151.6	9	1	197
Qy	162	198	151.6	9	1	198
Db	198	257	151.6	9	1	257
Qy	222	258	151.6	9	1	258
Db	282	318	151.6	9	1	318
Qy	342	378	151.6	9	1	378
Db	390	427	151.6	9	1	427

RESULT 13
 CL285168 1057 bp DNA linear GSS 10-FEB-2004
 DEFINITION ZMBB (HindIII) Zea mays genomic clone
 /note="genomic survey sequence."
 ACCESSION CL285168
 VERSION CL285168.1
 KEYWORDS GI:42499555
 SOURCE GSS
 ORGANISM Zea mays
 REFERENCES 1 (bases 1 to 1057)
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 TITLE Sequencing of the maize genome at PGIR (2003c)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Bharti,A.K.
 Dr.Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 405.
 Location/Qualifiers
 1..1057

FEATURES
 source

Query	Match	Length	Score	DB	Start	End
Qy	10.6%	161	151.6	9	1	161
Qy	68.3%	239	151.6	9	1	239
Db	0	109	151.6	9	1	109
Db	138	138	151.6	9	1	138
Qy	102	197	151.6	9	1	197
Qy	162	198	151.6	9	1	198
Db	198	257	151.6	9	1	257
Qy	222	258	151.6	9	1	258
Db	282	318	151.6	9	1	318
Qy	342	378	151.6	9	1	378
Db	390	427	151.6	9	1	427

RESULT 14
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 DEFINITION ZMBB (HindIII) Zea mays genomic clone
 /note="genomic survey sequence."
 ACCESSION CL291015
 VERSION CL291015.1
 KEYWORDS GI:42505402
 SOURCE GSS
 ORGANISM Zea mays
 REFERENCES 1 (bases 1 to 957)
 AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
 Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
 TITLE Sequencing of the maize genome at PGIR (2003c)
 JOURNAL Unpublished (2003)
 COMMENT Contact: Bharti,A.K.
 Dr.Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: SP6
 Class: BAC ends
 High quality sequence start: 399.
 Location/Qualifiers
 1..957

FEATURES
 source

Query	Match	Length	Score	DB	Start	End
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Qy	68.3%	239	151.6	9	1	239
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Db	138	138	151.6	9	1	138
Qy	102	197	151.6	9	1	197
Qy	162	198	151.6	9	1	198
Db	198	257	151.6	9	1	257
Qy	222	258	151.6	9	1	258
Db	282	318	151.6	9	1	318
Qy	342	378	151.6	9	1	378
Db	390	427	151.6	9	1	427

/clone_lib="Gossypium hirsutum L."
 /note="vector: pCTGBAC-1; Site 1: HindIII; Site 2: NotI;
 For more details on library preparation, ordering clones
 and sequence analysis see
http://www.genome.clemson.edu/projects/etc/cotton/GH_MBB"

ORIGIN

Query	Match	Score	DB	Length
Qy	Best Local Similarity 63.2% ;保守性 0 ; Mismatches 128 ; Indels 0 ; Gaps 0 ; Matches 220 ;	10.0%	8	569;
Qy	46 CTATGATTTCAGATTGCTAAAGACTCTPATCATAGAAGAGCCCTCAGAGGATCCC	105		
Db	364 CTTTGTGTTCAAATCGCATGGATCTGACATTCTGACTTAC	305		
Qy	106 AAATTAGCTAAATTATCCTCAAGCTCTGGAAACCACTCAGGACCCAAACCGTCGT	165		
Db	304 GGATACCCTTACTTCTGTTGGGATTTAATCAACTCCGAAAATTTCACRT	245		
Qy	166 CACCCNACTCAGTCTAAATAAACAGAGTATGACACTTATGACATTAAGGCCCTCGTAG	225		
Db	244 CACCGAGCTCGTCCAAACATGGTCAAAACATGGTCAAGGCTCTGGTAG	185		
Qy	226 GTGCCATCTGATGCGGAATGGAAACTGTATTGAGGGAACTCAACTACGGTAA	285		
Db	184 GTGCCATCTAACTTGTAAACTTGATGGAAACTTGTAAAGGAATTCAATAAGCTAA	125		
Qy	286 ATCCCTCAACTACTTCTAGTAAATCATAGCTCCAATCGTATCCTCTAGTAT	345		
- Db	124 ACCGTTCCCTGAACTACTGAACTCTGAGGGTGCACATCTCAACATTCCTCAAGTAC	65		
Qy	346 GAATCAGCTCTCAAATGGACATGGCTCGTCAAGGATGAAATGAGAC	393		
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RESULT 14
BH022375/c

LOCUS GH_MBb0002004r Gossypium hirsutum L. Gossypium hirsutum genomic clone GH_MBb0002004r, genomic survey sequence.

DEFINITION BH022375

VERSION 1

KEYWORDS GI:14576663

SOURCE GSS.

ORGANISM Gossypium hirsutum (upland cotton)

TITLE Gossypium hirsutum; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eu dicots; core eudicots; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE 1 (bases 1 to 686)

AUTHORS Tonkins,J.P., Peterson,D.G., Yang,T.J., Main,D., Wilkins,T.A., Paterson,A.H. and Wing,R.A.

JOURNAL Development of Genomic Resources for Cotton (Gossypium hirsutum L.); BAC Library Construction, Preliminary STC Analysis, and Identification of Clones Associated With Fiber Development Unpublished (2001)

COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu

FEATURES

source

/tissue_type="Young leaves"
 /lab_host="E. coli"
 /clone_lib="Gossypium hirsutum L."
 /note="Vector: pCTGBAC-1; Site 1: HindIII; Site 2: NotI;
 For more details on library preparation, ordering clones
 and sequence analysis see
http://www.genome.clemson.edu/projects/etc/cotton/GH_MBB"

ORIGIN

Query	Match	Score	DB	Length
Qy	Best Local Similarity 63.8% ;保守性 0 ; Mismatches 130 ; Indels 1 ; Gaps 1 ; Matches 231 ;	9.9%	8	686;
Qy	27 CCGGCTGTTGATCTATGATTTTCAGATTTGCAATCTATCTATCATTCATCAGAA	86		
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Qy	87 GACCCCTGAGAGATCCAAATTAGCTTAATTTATCCTCAGCTCTCGAAACACTCA	146		
Db	378 GAAACTTTAAATCATCACAGATACCCCTACTTTCCTGATTTCTAACAGACTCA	319		
Qy	147 GGACCCAAAACCCCTCGCTACCCAACTCAGTCATAATAACAGATGACACTTATGA	206		
Db	318 ACCCGTGAATCTATTCCTCTGAGCTCTGTCAGTACATAGTGGCATTTCT	259		
Qy	207 CCATAGAGCCCTGTAAGTGCAGATGCCGATCTAGATGCCGATTGAGCG	266		
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Db	78 AG 77			

RESULT 15
CC746178/c

LOCUS CC746178 DEFINITION 2NMBBb0122010.f 2NMBBb 2NMBBb0122010.5 ,
 genomic survey sequence.

ACCESSION CC746178
 VERSION CC746178.1
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Eukaryota; Viridiplanteae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Andropogoneae; Poales; Poaceae; clade; Panicoidae; Andropogoneae; Zea .
 REFERENCE 1 (bases 1 to 725)
 AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
 TITLE Sequencing of the maize genome
 JOURNAL Unpublished (2003)
 COMMENT Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 Tel: 520 626 3957
 Fax: 520 621 9288
 Email: <http://genome.arizona.edu>
 PCR Primers
 FORWARD: T7
 BACKWARD: M13r
 Plate: 0122 row: O column: 10
 Seq primer: T7

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Db	308 ATCGAAAGTGTTCAGATTAACATTTAACCTTTCTCACTCTTGATGTTGTCT	
Qy	140 CAACTCAGGACGCCAAAACCCGTGGCTCAGCCAACTCAGTCATAATAACAGAGTATCA	
Db	248 CAATCAACCCCGATAACCTTCTCTGACCTCACTCTTAACTAAGTTC	
Qy	200 CTTATGACCATATAGGCCCTAGGTAAAAATTCTCTGCAACTTCAATGAACTGTGA	
Db	188 CTTCGTGACCATACATGGCTCATACATGTCATTTTATGCTGATAACTGTTT	
Qy	260 GTAGCGGAACTCAACTAACGTTAAATTCTCTCAACTTCAATTGACCATGGCTCG	
Db	128 ATATGCGATTCACTATGGTGGAACTCTCTCCAACTTCAATTCTTAAATCTTAAACCA	
Qy	320 GCTTCAAAATGCTATGCTCTAGTATATGATATCA - CCTTCTCAATTGACCATGGCTCG	
Db	68 ATTCGGAACCATATCTTAAAGTATTGGATCATAGGATTCAAGTTCAGATTGACCATCTGCTG	
Qy	379 GATGGAA 385	
Db	A GATGAA 2	

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Job time : 7392 secs

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